EP/04/3984

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Patentanmeldung Nr. **Patent application No.** **Demande de brevet n°**

03450087.6

PRIORITY DOCUMENT

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Der Präsident des Europäischen Patentamts;
Im Auftrag

For the President of the European Patent Office

Le Président de l'Office européen des brevets
p.o.

R C van Dijk

Anmeldung Nr:
Application no.: 03450087.6
Demande no:

Anmeldetag:
Date of filing: 15.04.03
Date de dépôt:

Anmelder/Applicant(s)/Demandeur(s):

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Bezeichnung der Erfindung/Title of the invention/Titre de l'invention:
(Falls die Bezeichnung der Erfindung nicht angegeben ist, siehe Beschreibung.
If no title is shown please refer to the description.
Si aucun titre n'est indiqué se referer à la description.)

S. pneumoniae antigens

In Anspruch genommene Prioriät(en) / Priority(ies) claimed /Priorité(s) revendiquée(s)
Staat/Tag/Aktenzeichen/State/Date/File no./Pays/Date/Numéro de dépôt:

Internationale Patentklassifikation/International Patent Classification/
Classification internationale des brevets:

C07K14/00

Am Anmeldetag benannte Vertragstaaten/Contracting states designated at date of filing/Etats contractants désignées lors du dépôt:

AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HU IE IT LU MC NL
PT RO SE SI SK TR LI

The present invention relates to isolated nucleic acid molecules, which encode antigens for *Streptococcus pneumoniae*, which are suitable for use in preparation of pharmaceutical medicaments for the prevention and treatment of bacterial infections caused by *Streptococcus pneumoniae*.

Streptococcus pneumoniae (Pneumococcus) is a lancet-shaped, gram-positive, facultative anaerobic bacterium. It is only the encapsulated organism that is pathogenic for humans and experimental animals. Capsules are antigenic and form the basis for classifying pneumococci by serotypes. Ninety serotypes have been identified, based on their reaction with type-specific antisera. Most *S. pneumoniae* serotypes have been shown to cause serious disease, and the ten most common serotypes are estimated to account for about 62% of invasive disease worldwide. The ranking and serotype prevalence differs by age group and geographic area.

Pneumococci are common inhabitants of the respiratory tract, and may be isolated from the nasopharynx of 5% to 70% of normal adults. Rates of asymptomatic carriage vary with age, environment, and the presence of upper respiratory infections. Only 5%-10% of adults without children are carriers. In schools and orphanages, 27% to 58% of students and residents may be carriers. On military installations, as many as 50% to 60% of service personnel may be carriers. The duration of carriage varies and is generally longer in children than adults (reviewed in Epidemiology and Prevention of Vaccine-Preventable Diseases, 7th Edition-Second Printing, The Pink Book).

The relationship of carriage to the development of natural immunity is poorly understood. In addition, the immunologic mechanism that allows disease to occur in a carrier is poorly understood.

Streptococcus pneumoniae is an important agent of human disease at the extremities of age and in those who have underlying disease. Pneumococcal disease kills more people – in the US 40,000 or more each year – than all other vaccine preventable diseases combined. The major clinical syndromes of pneumococcal disease include pneumonia, bacteremia, and meningitis. The disease most often occurs when a predisposing condition exists, particularly pulmonary disease. It is a common bacterial complication of antecedent viral respiratory infection such as influenza and measles, and of chronic conditions such as chronic obstructive pulmonary disease, diabetes, congestive heart failure, renal failure, smoking and alcoholism. Pneumococcal infections are more common during the winter and in early spring when respiratory diseases are more prevalent. Immunodeficiency (splenic dysfunction, iatrogen, etc.) is a risk factor for development of fatal pneumococcal infections, because of decreased bacterial clearance and lack of antibodies. The incubation period is short, 1-3 days. Symptomes include an abrupt onset of fever and shaking chills or rigor, productive cough, pleuritic chest pain, dyspnoe, tachycardia and hypoxia.

S. pneumoniae is responsible for 88% of bacteremia infections in the US. Pneumonia is the most common form of invasive pneumococcal diseases: 150.000-570.000 cases per year (US). 36% of adult community-acquired and 50% of hospital-acquired pneumonia is caused by *S. pneumoniae* (US). The incidence of disease among adults aged 65 years and older has been reported to be ~60 cases/100.000. Case fatality rates for this disease increase from 1.4% for those aged two or younger to as high as 20.6% among those aged 80 or older. Diseases caused by influenza and *Pneumococcus* are together the fifth leading cause of death for persons aged 65 and older. Mortality attributable to these pathogens is more than 90% in this age group. Bacteremia occurs in about 25-30% of patients with pneumonia. The overall mortality rate of bacteremia is about 20%, but may be as high as 60% in elderly people. In 1998, 51% of all deaths attributable to invasive pneumococcal diseases occurred in age group above 65 years. Pneumococci cause 13%-19% of all cases of bacterial meningitis in the United States. An estimated 3,000 to 6,000 cases of pneumococcal meningitis occur each year. One-quarter of patients with pneumococcal meningitis also have pneumonia. The clinical symptoms, spinal fluid profile and neurologic complications are similar to other forms of purulent bacterial meningitis (reviewed in Epidemiology and Prevention of Vaccine-Preventable Diseases, 7th Edition-Second Printing, The Pink Book).

In children, Pneumococci are a common cause of acute otitis media, and are detected in 28%-55% of middle ear aspirates. By age 12 months, 62% of children have had at least one episode of acute otitis media. Middle ear infections are the most frequent reasons for pediatric office visits in the United States, resulting in over 20 million visits annually. Complications of pneumococcal otitis media may include mastoiditis and meningitis. Bacteremia without a known site of infection is the most common invasive clinical presentation among children <2 years of age, accounting for approximately 70% of invasive disease in this age group. Bacteremic pneumonia accounts for 12%-16% of invasive pneumococcal disease among children <2 years of age. With the decline of invasive Hib disease, *S. pneumoniae* has become the leading cause of bacterial meningitis among children <5 years of age in the United States. Children <1 year have the highest rates of pneumococcal meningitis, approximately 10 cases per 100,000 population. The burden of pneumococcal disease among children <5 years of age is significant. An estimated 17,000 cases of invasive disease occur each year, of which 13,000 are bacteremia without a known site of infection and about 700 are of meningitis. An estimated 200 children die every year as a result of invasive pneumococcal disease. Although not considered invasive disease, an estimated 5 million cases of acute otitis media occur each year among children <5 years of age (reviewed Epidemiology and Prevention of Vaccine-Preventable Diseases, 7th Edition-Second Printing, The Pink Book).

A definitive diagnosis of infection with *Streptococcus pneumoniae* generally relies on isolation of the organism from blood or other normally sterile body sites. Tests are also available to detect capsular polysaccharide antigen in body fluids.

Penicillin is the drug of choice for treatment. However, successful implementation of anti-infective therapy has become increasingly difficult because of widespread antimicrobial resistance. Resistance to penicillin is rising, and according to recent reports it reaches ~ 25% in the US {Whitney, C. et al., 2000}. The proportion of macrolide-resistant strains reached ~ 20 % {Hyde, T. et al., 2001}. Use of antimicrobial agents is highly correlated with the increase in resistance of *S. pneumoniae* to β-lactams and macrolides {McCormick, A. et al., 2003}.

However, even with effective antibiotic therapy (sensitive strains), the case fatality rate of invasive disease is high with an average of 10% in the developed world and can be much higher with certain serotypes, in elderly patients and in cases of bacteremia or meningitis (up to 80%).

Thus, there remains a need for an effective treatment to prevent or ameliorate spneumoococcal infections. A vaccine could not only prevent infections by streptococci, but more specifically prevent or ameliorate colonization of host tissues (esp. in nasopharynx), thereby reducing the incidence of upper respiratory infections and other suppurative infections, such otitis media. Elimination of invasive diseases - pneumonia, bacteremia and meningitis, and sepsis - would be a direct consequence of reducing the incidence of acute infection and carriage of the organism. Vaccines capable of showing cross-protection against the majority of *S. pneumoniae* strains causing human infections would also be useful to prevent or ameliorate infections caused by all other streptococcal species, namely groups A, B, C and G.

A vaccine can contain a whole variety of different antigens. Examples of antigens are whole-killed or attenuated organisms, subfractions of these organisms/tissues, proteins, or, in their most simple form, peptides. Antigens can also be recognized by the immune system in form of glycosylated proteins or peptides and may also be or contain polysaccharides or lipids. Short peptides can be used since for example cytotoxic T-cells (CTL) recognize antigens in form of short usually 8-11 amino acids long peptides in conjunction with major histocompatibility complex (MHC). B-cells can recognize linear epitopes as short as 4-5 amino acids, as well as three-dimensional structures (conformational epitopes). In order to obtain sustained, antigen-specific immune responses, adjuvants need to trigger immune cascades that involve all cells of the immune system. Primarily, adjuvants are acting, but are not restricted in their mode of action, on so-called antigen presenting cells (APCs). These cells usually first

encounter the antigen(s) followed by presentation of processed or unmodified antigen to immune effector cells. Intermediate cell types may also be involved. Only effector cells with the appropriate specificity are activated in a productive immune response. The adjuvant may also locally retain antigens and co-injected other factors. In addition the adjuvant may act as a chemoattractant for other immune cells or may act locally and/or systemically as a stimulating agent for the immune system.

Efforts to develop effective pneumococcal vaccines began as early as 1911. However, with the advent of penicillin in the 1940s, interest in the vaccine declined, until it was observed that many patients still died despite antibiotic treatment. By the late 60s, efforts were again being made to develop a polyvalent vaccine. The first pneumococcal vaccines contained purified capsular polysaccharide antigen from 14 different types of pneumococcal bacteria. In 1983, a 23-valent polysaccharide vaccine (PPV23) was licensed and replaced the 14- valent vaccine, which is no longer produced. PPV23 contains polysaccharide antigen from 23 types of pneumococcal bacteria which cause 88% of bacteremic pneumococcal disease. In addition, cross-reactivity occurs for several capsular types which account for an additional 8% of bacteremic disease. Two polysaccharide vaccines are available in the United States (Pneumovax 23, Merck, and Pnu-Immune 23, Wyeth-Lederle). Both vaccines contain 25 μg of each antigen per dose and include either phenol or thimerosal as a preservative.

The first pneumococcal conjugate vaccine (PCV7, Prevnar) was licensed in the United States in 2000. It includes purified capsular polysaccharide of 7 serotypes of *S. pneumoniae* (4, 9V, 14, 19F, 23F, 18C, and 6B) conjugated to a nontoxic variant of diphtheria toxin known as CRM197. The serotypes included in Prevnar accounted for 86% of bacteremia, 83% of meningitis, and 65% of acute otitis media among children <6 years of age in the United States during 1978-1994 (reviewed in Epidemiology and Prevention of Vaccine-Preventable Diseases, 7th Edition-Second Printing, The Pink Book). Additional pneumococcal polysaccharide conjugate vaccines containing 9 and 11 serotypes of *S. pneumoniae* are being developed. The vaccine is administered intramuscularly. After 4 doses of Prevnar vaccine, virtually all healthy infants develop antibody to all 7 serotypes contained in the vaccine. Prevnar has also been shown to be immunogenic in infants and children, including those with sickle cell disease and HIV infection. In a large clinical trial, Prevnar was shown to reduce invasive disease caused by vaccine serotypes, and reduce invasive disease caused by all serotypes, including serotypes not in the vaccine. Children who received Prevnar had fewer episodes of acute otitis media and underwent fewer tympanostomy tube placements than unvaccinated children. The duration of protection following Prevnar is currently unknown. Immunization with Prevnar reduces the rate of nasopharyngeal carriage of the vaccine serotypes, while the overall carriage rate is unaffected. Unfortunately, it has also been shown to induce serotype redistribution, that is the replacement of vaccine serotypes by strains, which are not covered by Prevnar {Pelton, S. et al., 2003}.

Pneumococcal vaccine is recommended to be administered routinely to i., all children as part of the routine shildhood immunization schedule, ii., adults 65 years of age and older and iii., persons aged >2 years with normal immune systems who have chronic illnesses, including cardiovascular disease, pulmonary disease, diabetes, alcoholism, cirrhosis, or cerebrospinal fluid leaks. In the elderly population the target groups for pneumococcal vaccine and influenza vaccine overlap. These vaccines can be given at the same time at different sites without increased side effects.

High mortality is observed among high-risk individuals (with underlying disease – mainly viral respiratory infection, immunocompromise) even with effective antibiotic therapy. The mAb approach targets patients with serious disease and provides immediate immune enhancement for the clearance of the bacteria. Through opsonization bacteria are killed within phagocytic cells and not lysed in the blood by antibiotics. This mechanism of action can help to eliminate the release of toxins (such as pneumolysin and other cytotoxins), which worsen the clinical condition of septic patients. Recent advances in the technology of monoclonal antibody production provide the means to generate human antibody reagents and reintroduce antibody therapies, while avoiding the toxicities associated with serum therapy.

Immunoglobulins are an extremely versatile class of antimicrobial proteins that can be used to prevent and treat emerging infectious diseases. Antibody therapy has been effective against a variety of diverse microorganisms reviewed in {Burnie, J. et al., 1998}.

Although capsular specific antibodies have been shown to be highly protective, it remains unclear what concentration of these serotype-specific antibodies protect against disease and more recently it has become clear that opsonic activity and avidity of these antibodies are more critical determinants of protection than concentration.

Protein conjugate vaccines are no doubt a great new addition to the amarmatorium in the battle against pneumococcal disease, but the vaccine contains a limited number of pneumococcal serotypes and given adequate ecological pressure, replacement disease by non-vaccine serotypes remains a real threat, particularly in areas with very high disease burden.

During the last decade the immunogenicity and protective capacity of several pneumococcal proteins have been described in animal models and these are now being explored for the development of species-common protein based vaccines. Such proteins are the Pneumococcal surface protein A (PspA, {McDaniel, L. et al., 1991}; {Roche, H. et al., 2003}), Pneumococcal surface adhesin A (PsaA, {Talkington, D. et al., 1996}), Choline binding protein A (CbpA, {Rosenow, C. et al., 1997}), LytB glucosaminidase, LytC muramidase, PrtA serine protease, PhtA (histidine triad A) and Pneumococcal vaccine antigen A (PvaA) {Wizemann, T. et al., 2001}; {Adamou, J. et al., 2001}.

Certain proteins or enzymes displayed on the surface of gram-positive organisms significantly contribute to pathogenesis, and might be involved in the disease process caused by these pathogens. Often, these proteins are involved in direct interactions with host tissues or in conceiling the bacterial surface from the host defense mechanisms {Navarre, W. et al., 1999}. *S. pneumoniae* is not an exception in this regard. Several surface proteins are characterized by as virulence factors, important for pneumococcal pathogenicity reviewed in {Jedrzejas, M., 2001}. If antibodies to these proteins could offer better protection to humans, they could provide the source of a novel, protein-based pneumococcal vaccine to be used in conjunction with or in place of the more traditional capsular polysaccharise vaccine. The use of some of the above-described proteins as antigens for a potential vaccine as well as a number of additional candidates reviewed in {Di Guilmi, A. et al., 2002} resulted mainly from a selection based on easiness of identification or chance of availability. There is a demand to identify relevant antigens for *S. pneumoniae* in a more comprehensive way.

The present inventors have developed a method for identification, isolation and production of hyperimmune serum reactive antigens from a specific pathogen, especially from *Staphylococcus aureus* and *Staphylococcus epidermidis* (WO 02/059148). However, given the differences in biological property, pathogenic function and genetic background, *Streptococcus pneumoniae* is distinctive from *Staphylococcus* strains. Importantly, the selection of sera for the identification of antigens from *S. pneumoniae* is different from that applied to the *S. aureus* screens. Three major types of human sera were collected for that purpose. First, healthy adults below <45 years of age preferably with small children in the household were tested for nasopharyngeal carriage of *S. pneumoniae*. A large percentage of young children are carriers of *S. pneumoniae*, and they are considered to be a source for exposure for their family members. Based on correlative data, protective (colonization neutralizing) antibodies are likely to be present in exposed individuals (children with high carriage rate in the household) who are not carriers of *S. pneumoniae*. To be able to select for relevant serum sources, a series of ELISAs measuring anti-*S. pneumoniae* IgG and IgA antibody levels were performed with bacterial lysates and culture supernatant proteins. Sera from high titer non-carriers were included in the genomic-based antigen identification. This approach for selection of human sera is basically very different from that used for *S. aureus*, where carriage or non-carriage state couldn't be associated with antibody levels. Second, serum samples from

convalescent phase patients with invasive pneumococcal diseases were characterized and selected in the same way. The third group of sera, containing longitudinally collected samples were also obtained from individuals with invasive disease and were used mainly for validation purposes. The main value of this collection is that one can follow the changes in antigen-specific antibody levels before diase (prae-), at the time of onset (acute) and during recovery (convalescent). This latter group helps in the selection of epitopes, which induce antibodies during disease and missing in the prae-disease state.

The genomes of the two bacterial species *S. pneumoniae* and *S. aureus* by itself show a number of important differences. The genome of *S. pneumoniae* contains app. 2.16 Mb, while *S. aureus* harbours 2.85 Mb. They have an average GC content of 39.7 and 33%, respectively and approximately 30 to 45% of the encoded genes are not shared between the two pathogens. In addition, the two bacterial species require different growth conditions and media for propagation. While *S. pneumoniae* is a strictly human pathogen, *S. aureus* can also be found infecting a range of warm-blooded animals. A list of the most important diseases, which can be inflicted by the two pathogens is presented below. *S. aureus* causes mainly nosocomial, opportunistic infections: impetigo, folliculitis, abscesses, boils, infected lacerations, endocarditis, meningitis, septic arthritis, pneumonia, osteomyelitis, scalded skin syndrome (SSS), toxic shock syndrome. *S. pneumoniae* causes mainly community aquired infections: upper (pharyngitis, otitis media) and and lower respiratory infections (pneumonia), as well as bacteremia, sepsis and meningitis.

The complete genome sequence of a capsular serotype 4 isolate of *S. pneumoniae*, designated TIGR4 was determined by the random shotgun sequencing strategy (GenBank accession number AE005672; see www.tigr.org/tigrscripts/CMR2/CMRHomePage.spl). This clinical isolate was taken from the blood of a 30-year-old male patient in Kongsvinger, Norway, and is highly invasive and virulent in a mouse model of infection.

The problem underlying the present invention was to provide means for the development of medicaments such as vaccines against *S. pneumoniae* infection. More particularly, the problem was to provide an efficient, relevant and comprehensive set of nucleic acid molecules or hyperimmune serum reactive antigens from *S. pneumoniae* that can be used for the manufacture of said medicaments.

Therefore, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence, which is selected from the group consisting of:

a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from **Seq ID No 1, 101-144.**
b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).

According to a preferred embodiment of the present invention the sequence identity is at least 80%, preferably at least 95%, especially 100%.

Furthermore, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of

a) a nucleic acid molecule having at least 96% sequence identity to a nucleic acid molecule selected from **Seq ID No** 2-6, 8, 10-16, 18-23, 25-31, 34, 36, 38-42, 44, 47-48, 51, 53, 55-62, 64, 67, 71-76, 78-79, 81-94, 96-100.

b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

According to another aspect, the present invention provides an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

a) a nucleic acid molecule selected from **Seq ID No** 9, 17, 24, 32, 37, 43, 52, 54, 65-66, 70, 80.
b) a nucleic acid molecule which is complementary to the nucleic acid of a),
c) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

Preferably, the nucleic acid molecule is DNA or RNA.

According to a preferred embodiment of the present invention, the nucleic acid molecule is isolated from a genomic DNA, especially from a S. *pneumoniae* genomic DNA.

According to the present invention a vector comprising a nucleic acid molecule according to any of the present invention is provided.

In a preferred embodiment the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragments thereof encoded by the nucleic acid molecule according to the present invention.

The present invention also provides a host cell comprising the vector according to the present invention.

According to another aspect the present invention further provides a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to the present invention.

In a preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of **Seq ID No** 145, 245-288.

In another preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of **Seq ID No** 146-150, 152, 154-160, 162-167, 169-175, 178, 180, 182-186, 188, 191-192, 195, 197, 199-206, 208, 211, 215-220, 222-223, 225-238, 240-244.

In a further preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of **Seq ID No** 153, 161, 168, 176, 181, 187, 196, 198, 209-210, 214, 224.

According to a further aspect the present invention provides fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 1; the serum reactive epitopes of Table 2, especially peptides comprising amino acids 4-11, 35-64, 66-76, 101-108, 111-119 and 57-114 of **Seq ID No** 145; 5-27, 32-64, 92-102, 107-113, 119-125, 133-139, 148-162, 177-187, 195-201, 207-214, 241-251, 254-269, 285-300, 302-309, 317-324, 332-357, 365-404, 411-425, 443-463, 470-477, 479-487, 506-512, 515-520, 532-547, 556-596, 603-610, 616-622, 624-629, 636-642, 646-665, 667-674, 687-692, 708-720, 734-739, 752-757, 798-820, 824-851, 856-865 and 732-763 of **Seq ID No** 146; 14-21, 36-44, 49-66, 102-127, 162-167, 177-196, 45-109 and 145-172 of **Seq ID No** 147; 17-35, 64-75, 81-92, 100-119, 125-172, 174-183, 214-

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The present invention also provides a process for producing a *S. pneumoniae* hyperimmune serum reactive antigen or a fragment thereof according to the present invention comprising expressing one or more of the nucleic acid molecules according to the present invention in a suitable expression system.

Moreover, the present invention provides a process for producing a cell, which expresses a *S pneumoniae* hyperimmune serum reactive antigen or a fragment thereof according to the present invention comprising transforming or transfecting a suitable host cell with the vector according to the present invention.

According to the present invention a pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof as defined in the present invention or a nucleic acid molecule as defined in the present invention is provided.

In a preferred embodiment the pharmaceutical composition further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, especially KLKLLLLLKLK, neuroactive compounds, especially human growth hormone, alumn, Freund's complete or incomplete adjuvants or combinations thereof.

In a more preferred embodiment the immunostimulatory substance is a combination of either a polycationic polymer and immunostimulatory deoxynucleotides or of a peptide containing at least two LysLeuLys motifs and immunostimulatory deoxynucleotides.

In a still more preferred embodiment the polycationic polymer is a polycationic peptide, especially polyarginine.

According to the present invention the use of a nucleic acid molecule according to the present invention or a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *S. pneumoniae* infection, is provided.

Also an antibody, or at least an effective part thereof, which binds at least to a selective part of the hyperimmune serum-reactive antigen or a fragment thereof according to the present invention, is provided herewith.

In a preferred embodiment the antibody is a monoclonal antibody.

In another preferred embodiment the effective part of the antibody comprises Fab fragments.

In a further preferred embodiment the antibody is a chimeric antibody.

In a still preferred embodiment the antibody is a humanized antibody.

The present invention also provides a hybridoma cell line, which produces an antibody according to the present invention.

Moreover, the present invention provids a method for producing an antibody according to the present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in the invention, to said animal,
- removing an antibody containing body fluid from said animal, and
- producing the antibody by subjecting said antibody containing body fluid to further purification steps.

Accordingly, the present invention also provides a method for producing an antibody according to the present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in the present invention, to said animal,
- removing the spleen or spleen cells from said animal,
- producing hybridoma cells of said spleen or spleen cells,
- selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
- producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.

The antibodies provided or produced according to the above methods may be used for the preparation of a medicament for treating or preventing *S. pneumoniae* infections.

According to another aspect the present invention provides an antagonist, which binds to a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention.

Such an antagonist capable of binding to a hyperimmune serum-reactive antigen or fragment thereof according to the present invention may be identified by a method comprising the following steps:

a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to the present invention with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment thereof; and
b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.

An antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention to its interaction partner may be identified by a method comprising the following steps:

a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to the present invention,
b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to the present invention,
c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form an interaction complex,

d) providing a candidate antagonist,

e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex,

f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.

The hyperimmune serum reactive antigens or fragments thereof according to the present invention may be used for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.

The present invention also provides a process for *in vitro* diagnosing a disease related to expression of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

The present invention also provides a process for *in vitro* diagnosis of a bacterial infection, especially a *S. pneumoniae* infection, comprising analyzing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

Moreover, the present invention provides the use of a hyperimmune serum reactive antigen or fragment thereof according to the present invention for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is an anticaline.

The present invention also provides the use of a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and spiegelmers.

The nucleic acid molecule according to the present invention may also be used for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

The present invention advantageously provides an efficient, relevant and comprehensive set of isolated nucleic acid molecules and their encoded hyperimmune serum reactive antigens or fragments thereof identified from *S. pneumoniae* using an antibody preparation from multiple human plasma pools and surface expression libraries derived from the genome of *S. pneumoniae*. Thus, the present invention fulfils a widely felt demand for *S. pneumoniae* antigens, vaccines, diagnostics and products useful in procedures for preparing antibodies and for identifying compounds effective against *S. pneumoniae* infection.

An effective vaccine should be composed of proteins or polypeptides, which are expressed by all strains and are able to induce high affinity, abundant antibodies against cell surface components of *S. pneumoniae*. The antibodies should be IgG1 and/or IgG3 for opsonization, and any IgG subtype and IgA for neutralisation of adherence and toxin action. A chemically defined vaccine must be definitely superior compared to a whole cell vaccine (attenuated or killed), since components of *S. pneumoniae*, which cross-react with human tissues or inhibit opsonization can be eliminated, and the individual proteins inducing protective antibodies and/or a protective immune response can be selected.

The approach, which has been employed for the present invention, is based on the interaction of pneumococcal proteins or peptides with the antibodies present in human sera. The antibodies produced against *S. pneumoniae* by the human immune system and present in human sera are indicative of the *in*

vivo expression of the antigenic proteins and their immunogenicity. In addition, the antigenic proteins as identified by the bacterial surface display expression libraries using pools of pre-selected sera, are processed in a second and third round of screening by individual selected or generated sera. Thus the present invention supplies an efficient, relevant, comprehensive set of pneumoococcal antigens as a pharmaceutical composition, especially a vaccine preventing infection by *S. pneumoniae*.

In the antigen identification program for identifying a comprehensive set of antigens according to the present invention, at least two different bacterial surface expression libraries are screened with several serum pools or plasma fractions or other pooled antibody containing body fluids (antibody pools). The antibody pools are derived from a serum collection, which has been tested against antigenic compounds of *S. pneumoniae*, such as whole cell extracts and culture supernatant proteins. Preferably, two distinct serum collections are used: 1. With very stable antibody repertoire: normal adults, clinically healthy people, who are non-carriers and overcame previous encounters or currently carriers of *S. pneumoniae* without acute disease and symptoms, 2. With antibodies induced acutely by the presence of the pathogenic organism: patients with acute disease with different manifestations (e.g. *S. pneumoniae* pharyngitis, pneumonia, bacteraemia, peritonitis, meningitis and sepsis). Sera have to react with multiple Pneumococcus-specific antigens in order to be considered hyperimmune and therefore relevant in the screening method applied for the present invention.

The expression libraries as used in the present invention should allow expression of all potential antigens, e.g. derived from all secreted and surface proteins of *S. pneumoniae*. Bacterial surface display libraries will be represented by a recombinant library of a bacterial host displaying a (total) set of expressed peptide sequences of *S. pneumoniae* on two selected outer membrane proteins (LamB and FhuA) at the bacterial host membrane {Georgiou, G., 1997}; {Etz, H. et al., 2001}. One of the advantages of using recombinant expression libraries is that the identified hyperimmune serum-reactive antigens may be instantly produced by expression of the coding sequences of the screened and selected clones expressing the hyperimmune serum-reactive antigens without further recombinant DNA technology or cloning steps necessary.

The comprehensive set of antigens identified by the described program according to the present invention is analysed further by one or more additional rounds of screening. Therefore individual antibody preparations or antibodies generated against selected peptides, which were identified as immunogenic are used. According to a preferred embodiment the individual antibody preparations for the second round of screening are derived from patients who have suffered from an acute infection with *S. pneumoniae*, especially from patients who show an antibody titer above a certain minimum level, for example an antibody titer being higher than 80 percentile, preferably higher than 90 percentile, especially higher than 95 percentile of the human (patient or healthy individual) sera tested. Using such high titer individual antibody preparations in the second screening round allows a very selective identification of the hyperimmune serum-reactive antigens and fragments thereof from *S. pneumoniae*.

Following the comprehensive screening procedure, the selected antigenic proteins, expressed as recombinant proteins or *in vitro* translated products, in case it can not be expressed in prokaryotic expression systems, or the identified antigenic peptides (produced synthetically) are tested in a second screening by a series of ELISA and Western blotting assays for the assessment of their immunogenicity with a large human serum collection (minimum ~150 healthy and patients sera).

It is important that the individual antibody preparations (which may also be the selected serum) allow a selective identification of the most promising candidates of all the hyperimmune serum-reactive antigens from all the promising candidates from the first round. Therefore, preferably at least 10 individual antibody preparations (i.e. antibody preparations (e.g. sera) from at least 10 different individuals having suffered from an infection to the chosen pathogen) should be used in identifying these antigens in the second screening round. Of course, it is possible to use also less than 10 individual preparations,

however, selectivity of the step may not be optimal with a low number of individual antibody preparations. On the other hand, if a given hyperimmune-serum-reactive-antigen (or an antigenic fragment thereof) is recognized by at least 10 individual antibody preparations, preferably at least 30, especially at least 50 individual antibody preparations, identification of the hyperimmune serum-reactive antigen is also selective enough for a proper identification. Hyperimmune serum-reactivity may of course be tested with as many individual preparations as possible (e.g. with more than 100 or even with more than 1,000).

Therefore, the relevant portion of the hyperimmune serum-reactive antibody preparations according to the method of the present invention should preferably be at least 10, more preferred at least 30, especially at least 50 individual antibody preparations. Alternatively (or in combination) hyperimmune serum-reactive antigens may preferably be also identified with at least 20%, preferably at least 30%, especially at least 40% of all individual antibody preparations used in the second screening round.

According to a preferred embodiment of the present invention, the sera from which the individual antibody preparations for the second round of screening are prepared (or which are used as antibody preparations), are selected by their titer against *S. pneumoniae* (e.g. against a preparation of this pathogen, such as a lysate, cell wall components and recombinant proteins). Preferably, some are selected with a total IgA titer above 2,000 U, especially above 4,000 U, and/or an IgG titer above 5,000 U, especially above 12,000 U (U = units, calculated from the OD_{405nm} reading at a given dilution) when the whole organism (total lysate or whole cells) is used as antigen in the ELISA.

The antibodies produced against streptococci by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. The recognition of linear epitopes recognized by serum antibodies can be based on sequences as short as 4-5 amino acids. Of course it does not necessarily mean that these short peptides are capable of inducing the given antibody *in vivo*. For that reason the defined epitopes, polypeptides and proteins are further to be tested in animals (mainly in mice) for their capacity to induce antibodies against the selected proteins in vivo.

The preferred antigens are located on the cell surface or are secreted, and are therefore accessible extracellularly. Antibodies against cell wall proteins are expected to serve multiple purposes: to inhibit adhesion, to interfere with nutrient acquisition, to inhibit immune evasion nand to promote phagocytosis {Hornef, M. et al., 2002}. Antibodies against secreted proteins are beneficial in neutralisation of their function as toxin or virulence component. It is also known that bacteria communicate with each other through secreted proteins. Neutralizing antibodies against these proteins will interrupt growth-promoting cross-talk between or within streptococcal species. Bioinformatic analyses (signal sequences, cell wall localisation signals, transmembrane domains) proved to be very useful in assessing cell surface localisation or secretion. The experimental approach includes the isolation of antibodies with the corresponding epitopes and proteins from human serum, and the generation of immune sera in mice against (poly)peptides selected by the bacterial surface display screens. These sera are then used in a third round of screening as reagents in the following assays: cell surface staining of *S. pneumoniae* grown under different conditions (FACS or microscopy), determination of neutralizing capacity (toxin, adherence), and promotion of opsonization and phagocytosis (*in vitro* phagocytosis assay).

For that purpose, bacterial *E. coli* clones are directly injected into mice and immune sera are taken and tested in the relevant in vitro assay for functional opsonic or neutralizing antibodies. Alternatively, specific antibodies may be purified from human or mouse sera using peptides or proteins as substrate.

Host defence against *S. pneumoniae* relies mainly on opsonophagocytic killing mechanism. Inducing high affinity antibodies of the opsonic and neutralizing type by vaccination helps the innate immune system to eliminate bacteria and toxins. This makes the method according to the present invention an optimal tool

for the identification of pneumococcal antigenic proteins.

The skin and mucous membranes are formidable barriers against invasion by streptococci. However, once the skin or the mucous membranes are breached the first line of non-adaptive cellular defence begins its co-ordinate action through complement and phagocytes, especially the polymorphonuclear leukocytes (PMNs). These cells can be regarded as the cornerstones in eliminating invading bacteria. As *Streptococcus pneumoniae* is a primarily extracellular pathogen, the major anti-streptococcal adaptive response comes from the humoral arm of the immune system, and is mediated through three major mechanisms: promotion of opsonization, toxin neutralisation, and inhibition of adherence. It is believed that opsonization is especially important, because of its requirement for an effective phagocytosis. For efficient opsonization the microbial surface has to be coated with antibodies and complement factors for recognition by PMNs through receptors to the Fc fragment of the IgG molecule or to activated C3b. After opsonization, streptococci are phagocytosed and killed. Antibodies bound to specific antigens on the cell surface of bacteria serve as ligands for the attachment to PMNs and to promote phagocytosis. The very same antibodies bound to the adhesins and other cell surface proteins are expected to neutralize adhesion and prevent colonization. The selection of antigens as provided by the present invention is thus well suited to identify those that will lead to protection against infection in an animal model or in humans.

According to the antigen identification method used herein, the present invention can surprisingly provide a set of comprehensive novel nucleic acids and novel hyperimmune serum reactive antigens and fragments thereof of *S. pneumoniae*, among other things, as described below. According to one aspect, the invention particularly relates to the nucleotide sequences encoding hyperimmune serum reactive antigens which sequences are set forth in the Sequence listing **Seq ID No**: 1-144 and the corresponding encoded amino acid sequences representing hyperimmune serum reactive antigens are set forth in the Sequence Listing **Seq ID No** 145-288.

In a preferred embodiment of the present invention, a nucleic acid molecule is provided which exhibits 70% identity over their entire length to a nucleotide sequence set forth with **Seq ID No** 1, 101-144. Most highly preferred are nucleic acids that comprise a region that is at least 80% or at least 85% identical over their entire length to a nucleic acid molecule set forth with **Seq ID No** 1, 101-144. In this regard, nucleic acid molecules at least 90%, 91%, 92%, 93%, 94%, 95%, or 96% identical over their entire length to the same are particularly preferred. Furthermore, those with at least 97% are highly preferred, those with at least 98% and at least 99% are particularly highly preferred, with at least 99% or 99.5% being the more preferred, with 100% identity being especially preferred. Moreover, preferred embodiments in this respect are nucleic acids which encode hyperimmune serum reactive antigens or fragments thereof (polypeptides) which retain substantially the same biological function or activity as the mature polypeptide encoded by said nucleic acids set forth in the **Seq ID No** 1, 101-144.

Identity, as known in the art and used herein, is the relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, identity also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. Identity can be readily calculated. While there exist a number of methods to measure identity between two polynucleotide or two polypeptide sequences, the term is well known to skilled artisans (e.g. *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity are codified in computer programs. Preferred computer program methods to determine identity between two sequences include, but are not limited to, GCG program package {Devereux, J. et al., 1984}, BLASTP, BLASTN, and FASTA {Altschul, S. et al., 1990}.

According to another aspect of the invention, nucleic acid molecules are provided which exhibit at least 96% identity to the nucleic acid sequence set forth with **Seq ID No** 2-6, 8, 10-16, 18-23, 25-31, 34, 36, 38-42,

44, 47-48, 51, 53, 55-62, 64, 67, 71-76, 78-79, 81-94, 96-100.

According to a further aspect of the present invention, nucleic acid molecules are provided which are identical to the nucleic acid sequences set forth with **Seq ID No** 9, 17, 24, 32, 37, 43, 52, 54, 65-66, 70, 80.

The nucleic acid molecules according to the present invention can as a second alternative also be a nucleic acid molecule which is at least essentially complementary to the nucleic acid described as the first alternative above. As used herein complementary means that a nucleic acid strand is base pairing via Watson-Crick base pairing with a second nucleic acid strand. Essentially complementary as used herein means that the base pairing is not occurring for all of the bases of the respective strands but leaves a certain number or percentage of the bases unpaired or wrongly paired. The percentage of correctly pairing bases is preferably at least 70 %, more preferably 80 %, even more preferably 90 % and most preferably any percentage higher than 90 %. It is to be noted that a percentage of 70 % matching bases is considered as homology and the hybridization having this extent of matching base pairs is considered as stringent. Hybridization conditions for this kind of stringent hybridization may be taken from Current Protocols in Molecular Biology (John Wiley and Sons, Inc., 1987). More particularly, the hybridization conditions can be as follows:

- Hybridization performed e.g. in 5 x SSPE, 5 x Denhardt's reagent, 0.1% SDS, 100 g/mL sheared DNA at 68°C
- Moderate stringency wash in 0.2xSSC, O.1% SDS at 42°C
- High stringency wash in 0.1xSSC, 0.1% SDS at 68°C

Genomic DNA with a GC content of 50% has an approximate T_M of 96°C. For 1% mismatch, the T_M is reduced by approximately 1°C.

In addition, any of the further hybridization conditions described herein are in principle applicable as well.

Of course, all nucleic acid sequence molecules which encode the same polypeptide molecule as those identified by the present invention are encompassed by any disclosure of a given coding sequence, since the degeneracy of the genetic code is directly applicable to unambiguously determine all possible nucleic acid molecules which encode a given polypeptide molecule, even if the number of such degenerated nucleic acid molecules may be high. This is also applicable for fragments of a given polypeptide, as long as the fragments encode a polypeptide being suitable to be used in a vaccination connection, e.g. as an active or passive vaccine.

The nucleic acid molecule according to the present invention can as a third alternative also be a nucleic acid which comprises a stretch of at least 15 bases of the nucleic acid molecule according to the first and second alternative of the nucleic acid molecules according to the present invention as outlined above. Preferably, the bases form a contiguous stretch of bases. However, it is also within the scope of the present invention that the stretch consists of two or more moieties, which are separated by a number of bases.

The present nucleic acids may preferably consist of at least 20, even more preferred at least 30, especially at least 50 contiguous bases from the sequences disclosed herein. The suitable length may easily be optimized due to the planned area of use (e.g. as (PCR) primers, probes, capture molecules (e.g. on a (DNA) chip), etc.). Preferred nucleic acid molecules contain at least a contiguous 15 base portion of one or more of the predicted immunogenic amino acid sequences listed in tables 1 and 2, especially the sequences of table 2 with scores of more than 10, preferably more than 20, especially with a score of more than 25. Specifically preferred are nucleic acids containing a contiguous portion of a DNA sequence of any sequence in the sequence protocol of the present application which shows 1 or more, preferably more

than 2, especially more than 5, non-identical nucleic acid residues compared to the published *Streptococcus pneumoniae* strain TIGR4 genome ({Tettelin, H. et al., 2001}; GenBank accession AE005672) and/or any other published *S. pneumoniae* genome sequence or parts thereof, especially of the strain R6 ({Hoskins, J. et al., 2001}; GenBank accession AE007317). Specifically preferred non-identical nucleic acid residues are residues, which lead to a non-identical amino acid residue. Preferably, the nucleic acid sequences encode for polypeptides having at least 1, preferably at least 2, preferably at least 3 different amino acid residues compared to the published *S. pneumoniae* counterparts mentioned above. Also such isolated polypeptides, being fragments of the proteins (or the whole protein) mentioned herein e.g. in the sequence listing, having at least 6, 7, or 8 amino acid residues and being encoded by these nucleic acids are preferred.

The nucleic acid molecule according to the present invention can as a fourth alternative also be a nucleic acid molecule which anneals under stringent hybridisation conditions to any of the nucleic acids of the present invention according to the above outlined first, second, and third alternative. Stringent hybridisation conditions are typically those described herein.

Finally, the nucleic acid molecule according to the present invention can as a fifth alternative also be a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to any of the nucleic acid molecules according to any nucleic acid molecule of the present invention according to the first, second, third, and fourth alternative as outlined above. This kind of nucleic acid molecule refers to the fact that preferably the nucleic acids according to the present invention code for the hyperimmune serum reactive antigens or fragments thereof according to the present invention. This kind of nucleic acid molecule is particularly useful in the detection of a nucleic acid molecule according to the present invention and thus the diagnosis of the respective microorganisms such as *S. pneumoniae* and any disease or diseased condition where this kind of microorganims is involved. Preferably, the hybridisation would occur or be preformed under stringent conditions as described in connection with the fourth alternative described above.

Nucleic acid molecule as used herein generally refers to any ribonucleic acid molecule or deoxyribonucleic acid molecule, which may be unmodified RNA or DNA or modified RNA or DNA. Thus, for instance, nucleic acid molecule as used herein refers to, among other, single-and double-stranded DNA, DNA that is a mixture of single- and double-stranded RNA, and RNA that is a mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded, or triple-stranded, or a mixture of single- and double-stranded regions. In addition, nucleic acid molecule as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. As used herein, the term nucleic acid molecule includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "nucleic acid molecule" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are nucleic acid molecule as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term nucleic acid molecule as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of nucleic acid molecule, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple and complex cells, *inter alia*. The term nucleic acid molecule also embraces short nucleic acid molecules often referred to as oligonucleotide(s). "Polynucleotide" and "nucleic acid" or "nucleic acid molecule" are often used interchangeably herein.

Nucleic acid molecules provided in the present invention also encompass numerous unique fragments,

both longer and shorter than the nucleic acid molecule sequences set forth in the sequencing listing of the *S. pneumoniae* coding regions, which can be generated by standard cloning methods. To be unique, a fragment must be of sufficient size to distinguish it from other known nucleic acid sequences, most readily determined by comparing any selected *S. pneumoniae* fragment to the nucleotide sequences in computer databases such as GenBank.

Additionally, modifications can be made to the nucleic acid molecules and polypeptides that are encompassed by the present invention. For example, nucleotide substitutions can be made which do not affect the polypeptide encoded by the nucleic acid, and thus any nucleic acid molecule which encodes a hyperimmune serum reactive antigen or fragments thereof is encompassed by the present invention.

Furthermore, any of the nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof provided by the present invention can be functionally linked, using standard techniques such as standard cloning techniques, to any desired regulatory sequences, whether a *S. pneumoniae* regulatory sequence or a heterologous regulatory sequence, heterologous leader sequence, heterologous marker sequence or a heterologous coding sequence to create a fusion protein.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA or cRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced by chemical synthetic techniques or by a combination thereof. The DNA may be triple-stranded, double-stranded or single-stranded. Single-stranded DNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

The present invention further relates to variants of the herein above described nucleic acid molecules which encode fragments, analogs and derivatives of the hyperimmune serum reactive antigens and fragments thereof having a deducted *S. pneumoniae* amino acid sequence set forth in the Sequence Listing. A variant of the nucleic acid molecule may be a naturally occurring variant such as a naturally occurring allelic variant, or it may be a variant that is not known to occur naturally. Such non-naturally occurring variants of the nucleic acid molecule may be made by mutagenesis techniques, including those applied to nucleic acid molecules, cells or organisms.

Among variants in this regard are variants that differ from the aforementioned nucleic acid molecules by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more nucleotides. The variants may be altered in coding or non-coding regions or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Preferred are nucleic acid molecules encoding a variant, analog, derivative or fragment, or a variant, analogue or derivative of a fragment, which have a *S. pneumoniae* sequence as set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid(s) is substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *S. pneumoniae* polypeptides set forth in the Sequence Listing. Also especially preferred in this regard are conservative substitutions.

The peptides and fragments according to the present invention also include modified epitopes wherein preferably one or two of the amino acids of a given epitope are modified or replaced according to the rules disclosed in e.g. (Tourdot, S. et al., 2000), as well as the nucleic acid sequences encoding such modified epitopes.

It is clear that also epitopes derived from the present epitopes by amino acid exchanges improving, conserving or at least not significantly impeding the T cell activating capability of the epitopes are covered by the epitopes according to the present invention. Therefore the present epitopes also cover epitopes, which do not contain the original sequence as derived from *S. pneumoniae*, but trigger the same or preferably an improved T cell response. These epitope are referred to as "heteroclitic"; they need to

have a similar or preferably greater affinity to MHC/HLA molecules, and the need the ability to stimulate the T cell receptors (TCR) directed to the original epitope in a similar or preferably stronger manner.

Heteroclitic epitopes can be obtained by rational design i.e. taking into account the contribution of individual residues to binding to MHC/HLA as for instance described by {Rammensee, H. et al., 1999}, combined with a systematic exchange of residues potentially interacting with the TCR and testing the resulting sequences with T cells directed against the original epitope. Such a design is possible for a skilled man in the art without much experimentation.

Another possibility includes the screening of peptide libraries with T cells directed against the original epitope. A preferred way is the positional scanning of synthetic peptide libraries. Such approaches have been described in detail for instance by {Hemmer, B. et al., 1999}and the references given therein.

As an alternative to epitopes represented by the present derived amino acid sequences or heteroclitic epitopes, also substances mimicking these epitopes e.g. "peptidemimetica" or "retro-inverso-peptides" can be applied.

Another aspect of the design of improved epitopes is their formulation or modification with substances increasing their capacity to stimulate T cells. These include T helper cell epitopes, lipids or liposomes or preferred modifications as described in WO 01/78767.

Another way to increase the T cell stimulating capacity of epitopes is their formulation with immune stimulating substances for instance cytokines or chemokines like interleukin-2, -7, -12, -18, class I and II interferons (IFN), especially IFN-gamma, GM-CSF, TNF-alpha, flt3-ligand and others.

As discussed additionally herein regarding nucleic acid molecule assays of the invention, for instance, nucleic acid molecules of the invention as discussed above, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes that have a high sequence similarity to the nucleic acid molecules of the present invention. Such probes generally will comprise at least 15 bases. Preferably, such probes will have at least 20, at least 25 or at least 30 bases, and may have at least 50 bases. Particularly preferred probes will have at least 30 bases, and will have 50 bases or less, such as 30, 35, 40, 45, or 50 bases.

For example, the coding region of a nucleic acid molecule of the present invention may be isolated by screening a relevant library using the known DNA sequence to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the present invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine to which members of the library the probe hybridizes.

The nucleic acid molecules and polypeptides of the present invention may be employed as reagents and materials for development of treatments of and diagnostics for disease, particularly human disease, as further discussed herein relating to nucleic acid molecule assays, *inter alia*.

The nucleic acid molecules of the present invention that are oligonucleotides can be used in the processes herein as described, but preferably for PCR, to determine whether or not the *S. pneumoniae* genes identified herein in whole or in part are present and/or transcribed in infected tissue such as blood. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. For this and other purposes the arrays comprising at least one of the nucleic acids according to the present invention as described herein, may be used.

The nucleic acid molecules according to the present invention may be used for the detection of nucleic acid molecules and organisms or samples containing these nucleic acids. Preferably such detection is for diagnosis, more preferable for the diagnosis of a disease related or linked to the present or abundance of *S. pneumoniae*.

Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with *S. pneumoniae* may be identifiable by detecting any of the nucleic acid molecules according to the present invention detected at the DNA level by a variety of techniques. Preferred nucleic acid molecules candidates for distinguishing a *S. pneumoniae* from other organisms can be obtained.

The invention provides a process for diagnosing disease, arising from infection with *S. pneumoniae*, comprising determining from a sample isolated or derived from an individual an increased level of expression of a nucleic acid molecule having the sequence of a nucleic acid molecule set forth in the Sequence Listing. Expression of nucleic acid molecules can be measured using any one of the methods well known in the art for the quantitation of nucleic acid molecules, such as, for example, PCR, RT-PCR, Rnase protection, Northern blotting, other hybridisation methods and the arrays described herein.

Isolated as used herein means separated "by the hand of man" from its natural state; i.e., that, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a naturally occurring nucleic acid molecule or a polypeptide naturally present in a living organism in its natural state is not "isolated," but the same nucleic acid molecule or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein. As part of or following isolation, such nucleic acid molecules can be joined to other nucleic acid molecules, such as DNAs, for mutagenesis, to form fusion proteins, and for propagation or expression in a host, for instance. The isolated nucleic acid molecules, alone or joined to other nucleic acid molecules such as vectors, can be introduced into host cells, in culture or in whole organisms. Introduced into host cells in culture or in whole organisms, such DNAs still would be isolated, as the term is used herein, because they would not be in their naturally occurring form or environment. Similarly, the nucleic acid molecules and polypeptides may occur in a composition, such as a media formulations, solutions for introduction of nucleic acid molecules or polypeptides, for example, into cells, compositions or solutions for chemical or enzymatic reactions, for instance, which are not naturally occurring compositions, and, therein remain isolated nucleic acid molecules or polypeptides within the meaning of that term as it is employed herein.

The nucleic acids according to the present invention may be chemically synthesized. Alternatively, the nucleic acids can be isolated from *S. pneumoniae* by methods known to the one skilled in the art.

According to another aspect of the present invention, a comprehensive set of novel hyperimmune serum reactive antigens and fragments thereof are provided by using the herein described antigen identification method. In a preferred embodiment of the invention, a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by any one of the nucleic acids molecules herein described and fragments thereof are provided. In another preferred embodiment of the invention a novel set of hyperimmune serum-reactive antigens which comprises amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 145, 245-288 and fragments thereof are provided. In a further preferred embodiment of the invention hyperimmune serum-reactive antigens which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 146-150, 152, 154-160, 162-167, 169-175, 178, 180, 182-186, 188, 191-192, 195, 197, 199-206, 208, 211, 215-220, 222-223, 225-238, 240-244 and fragments thereof are provided. In a still preferred embodiment of the invention hyperimmune serum-reactive antigens which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 153, 161, 168, 176, 181, 187, 196, 198, 209-210, 214, 224 and fragments thereof are provided.

The hyperimmune serum reactive antigens and fragments thereof as provided in the invention include

any polypeptide set forth in the Sequence Listing as well as polypeptides which have at least 70% identity to a polypeptide set forth in the Sequence Listing, preferably at least 80% or 85% identity to a polypeptide set forth in the Sequence Listing, and more preferably at least 90% similarity (more preferably at least 90% identity) to a polypeptide set forth in the Sequence Listing and still more preferably at least 95%, 96%, 97%, 98%, 99% or 99.5% similarity (still more preferably at least 95%, 96%, 97%, 98%, 99%, or 99.5% identity) to a polypeptide set forth in the Sequence Listing and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 4 amino acids and more preferably at least 8, still more preferably at least 30, still more preferably at least 50 amino acids, such as 4, 8, 10, 20, 30, 35, 40, 45 or 50 amino acids.

The invention also relates to fragments, analogs, and derivatives of these hyperimmune serum reactive antigens and fragments thereof. The terms "fragment", "derivative" and "analog" when referring to an antigen whose amino acid sequence is set forth in the Sequence Listing, means a polypeptide which retains essentially the same or a similar biological function or activity as such hyperimmune serum reactive antigen and fragment thereof.

The fragment, derivative or analog of a hyperimmune serum reactive antigen and fragment thereof may be 1) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or 2) one in which one or more of the amino acid residues includes a substituent group, or 3) one in which the mature hyperimmune serum reactive antigen or fragment thereof is fused with another compound, such as a compound to increase the half-life of the hyperimmune serum reactive antigen and fragment thereof (for example, polyethylene glycol), or 4) one in which the additional amino acids are fused to the mature hyperimmune serum reactive antigen or fragment thereof, such as a leader or secretory sequence or a sequence which is employed for purification of the mature hyperimmune serum reactive antigen or fragment thereof or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

The present invention also relates to antigens of different *S. pneumoniae* isolates. Such homologues may easily be isolated based on the nucleic acid and amino acid sequences disclosed herein. There are more than 90 serotypes in more than 40 serogroups distinguished to date and the typing is based on serotype specific antisera. The presence of any antigen can accordingly be determined for every serotype. In addition it is possible to determine the variability of a particular antigen in the various serotypes as described for the *S. pyogenes* sic gene {Hoe, N. et al., 2001}. The contribution of the various serotypes to the different pneumococcal infections varies in the different age groups and geographical regions {Gray, B. et al., 1979}; {Gray, B. et al., 1986}; {Orange, M. et al., 1993}, reviewed in Epidemiology and Prevention of Vaccine-Preventable Diseases, 7th Edition-Second Printing, The Pink Book). It is an important aspect that the most valuable protective antigens are expected to be conserved among various clinical strains.

Among the particularly preferred embodiments of the invention in this regard are the hyperimmune serum reactive antigens set forth in the Sequence Listing, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of fragments. Additionally, fusion polypeptides comprising such hyperimmune serum reactive antigens, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of the fragments are also encompassed by the present invention. Such fusion polypeptides and proteins, as well as nucleic acid molecules encoding them, can readily be made using standard techniques, including standard recombinant techniques for producing and expression of a recombinant polynucleic acid encoding a fusion protein.

Among preferred variants are those that vary from a reference by conservative amino acid substitutions. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the replacements, one for another,

among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr.

Further particularly preferred in this regard are variants, analogs, derivatives and fragments, and variants, analogs and derivatives of the fragments, having the amino acid sequence of any polypeptide set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the polypeptide of the present invention. Also especially preferred in this regard are conservative substitutions. Most highly preferred are polypeptides having an amino acid sequence set forth in the Sequence Listing without substitutions.

The hyperimmune serum reactive antigens and fragments thereof of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

Also among preferred embodiments of the present invention are polypeptides comprising fragments of the polypeptides having the amino acid sequence set forth in the Sequence Listing, and fragments of variants and derivatives of the polypeptides set forth in the Sequence Listing.

In this regard a fragment is a polypeptide having an amino acid sequence that entirely is the same as part but not all of the amino acid sequence of the afore mentioned hyperimmune serum reactive antigen and fragment thereof, and variants or derivative, analogs, fragments thereof. Such fragments may be "free-standing", i.e., not part of or fused to other amino acids or polypeptides, or they may be comprised within a larger polypeptide of which they form a part or region. Also preferred in this aspect of the invention are fragments characterised by structural or functional attributes of the polypeptide of the present invention, i.e. fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta-amphipathic regions, flexible regions, surface-forming regions, substrate binding regions, and high antigenic index regions of the polypeptide of the present invention, and combinations of such fragments. Preferred regions are those that mediate activities of the hyperimmune serum reactive antigens and fragments thereof of the present invention. Most highly preferred in this regard are fragments that have a chemical, biological or other activity of the hyperimmune serum reactive antigen and fragments thereof of the present invention, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Particularly preferred are fragments comprising receptors or domains of enzymes that confer a function essential for viability of *S. pneumoniae* or the ability to cause disease in humans. Further preferred polypeptide fragments are those that comprise or contain antigenic or immunogenic determinants in an animal, especially in a human.

An antigenic fragment is defined as a fragment of the identified antigen, which is for itself antigenic or may be made antigenic when provided as a hapten. Therefore, also antigens or antigenic fragments showing one or (for longer fragments) only a few amino acid exchanges are enabled with the present invention, provided that the antigenic capacities of such fragments with amino acid exchanges are not severely deteriorated on the exchange(s), i.e., suited for eliciting an appropriate immune response in an individual vaccinated with this antigen and identified by individual antibody preparations from individual sera.

Preferred examples of such fragments of a hyperimmune serum-reactive antigen are selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa", and "Location of identified immunogenic region" of Table 1; the serum reactive epitopes of Table 2, especially peptides comprising amino acid 4-11, 35-64, 66-76, 101-108, 111-119 and 57-114 of Seq ID No

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178; 184-200, 367-388, 382-403, 409-429, 425-444 and 438-457 of Seq ID No 179; 27-50 and 45-67 of Seq ID No 180; 114-131 and 405-419 of Seq ID No 183; 113-134, 129-150, 145-166, 161-182 and 177-198 of Seq ID No 184; 495-515 of Seq ID No 186; 346-358 of Seq ID No 187; 208-224 of Seq ID No 190; 178-194, 202-223, 217- 238, 288-308 and 1355-1372 of Seq ID No 192; 57-78 of Seq ID No 194; 347-369, 364-386, 381-403, 398-420, 415-437 and 432-452 of Seq ID No 197; 347-372 of Seq ID No 198; 147-163 of Seq ID No 199; 263-288 of Seq ID No 200; 361-377 of Seq ID No 202; 82-104, 99-121, 116-138, 133-155 and 150-171 of Seq ID No 204; 110-130 and 125-145 of Seq ID No 205; 613-631, 626-644 and 196-213 of Seq ID No 206; 78-100, 95-117, 112-134 and 129-151 of Seq ID No 208; 158-180, 175-197, 192-214, 209-231 and 226-248 of Seq ID No 209; 30-50, 45-65 and 60-79 of Seq ID No 210; 431-455 and 450-474 of Seq ID No 213; 579-601, 596-618, 613-635 and 630-653 of Seq ID No 214; 920-927, 98-119, 114-135, 130-151, 146-167 and 162-182 of Seq ID No 217; 36-59 of Seq ID No 219; 194-216 and 381-404 of Seq ID No 220; 236-251 and 255-279 of Seq ID No 221; 80-100 and 141-164 of Seq ID No 222; 128-154 of Seq ID No 223; 82-100, 95-116 and 111-134 of Seq ID No 224; 55-76, 71-92 and 87-110 of Seq ID No 227; 91-106 of Seq ID No 229; 74-96 of Seq ID No 230; 140-157 of Seq ID No 231; 4-13 of Seq ID No 233; 41-65 and 499-523 of Seq ID No 236; 122-146, 191-215, 288-313, 445-469 and 511-535 of Seq ID No 239; 347-368 of Seq ID No 241; 46-61 of Seq ID No 242; 15-37, 32-57, 101-121, 115-135, 138-158, 152-172, 220-242 and 236-258 of Seq ID No 243, and fragments comprising at least 6, preferably more than 8, especially more than 10 aa of said sequences. All these fragments individually and each independently form a preferred selected aspect of the present invention.

All linear hyperimmune serum reactive fragments of a particular antigen may be identified by analysing the entire sequence of the protein antigen by a set of peptides overlapping by 1 amino acid with a length of at least 10 amino acids. Subsequently, non-linear epitopes can be identified by analysis of the protein antigen with hyperimmune sera using the expressed full-length protein or domain polypeptides thereof. Assuming that a distinct domain of a protein is sufficient to form the 3D structure independent from the native protein, the analysis of the respective recombinant or synthetically produced domain polypeptide with hyperimmune serum would allow the identification of conformational epitopes within the individual domains of multi-domain proteins. For those antigens where a domain possesses linear as well as conformational epitopes, competition experiments with peptides corresponding to the linear epitopes may be used to confirm the presence of conformational epitopes.

It will be appreciated that the invention also relates to, among others, nucleic acid molecules encoding the aforementioned fragments, nucleic acid molecules that hybridise to nucleic acid molecules encoding the fragments, particularly those that hybridise under stringent conditions, and nucleic acid molecules, such as PCR primers, for amplifying nucleic acid molecules that encode the fragments. In these regards, preferred nucleic acid molecules are those that correspond to the preferred fragments, as discussed above.

The present invention also relates to vectors, which comprise a nucleic acid molecule or nucleic acid molecules of the present invention, host cells which are genetically engineered with vectors of the invention and the production of hyperimmune serum reactive antigens and fragments thereof by recombinant techniques.

A great variety of expression vectors can be used to express a hyperimmune serum reactive antigen or fragment thereof according to the present invention. Generally, any vector suitable to maintain, propagate or express nucleic acids to express a polypeptide in a host may be used for expression in this regard. In accordance with this aspect of the invention the vector may be, for example, a plasmid vector, a single or double-stranded phage vector, a single or double-stranded RNA or DNA viral vector. Starting plasmids disclosed herein are either commercially available, publicly available, or can be constructed from available plasmids by routine application of well-known, published procedures. Preferred among vectors, in certain respects, are those for expression of nucleic acid molecules and hyperimmune serum reactive antigens or fragments thereof of the present invention. Nucleic acid constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence.

Alternatively, the hyperimmune serum reactive antigens and fragments thereof of the invention can be synthetically produced by conventional peptide synthesizers. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA construct of the present invention.

Host cells can be genetically engineered to incorporate nucleic acid molecules and express nucleic acid molecules of the present invention. Representative examples of appropriate hosts include bacterial cells, such as streptococci, staphylococci, *E. coli*, *Streptomyces* and *Bacillus subtillis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, Hela, C127, 3T3, BHK, 293 and Bowes melanoma cells; and plant cells.

The invention also provides a process for producing a *S. pneumoniae* hyperimmune serum reactive antigen and a fragment thereof comprising expressing from the host cell a hyperimmune serum reactive antigen or fragment thereof encoded by the nucleic acid molecules provided by the present invention. The invention further provides a process for producing a cell, which expresses a *S. pneumoniae* hyperimmune serum reactive antigen or a fragment thereof comprising transforming or transfecting a suitable host cell with the vector according to the present invention such that the transformed or transfected cell expresses the polypeptide encoded by the nucleic acid contained in the vector.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals but also additional heterologous functional regions. Thus, for instance, a region of additional amino acids, particularly charged amino acids, may be added to the N- or C-terminus of the polypeptide to improve stability and persistence in the host cell, during purification or during subsequent handling and storage. Also, regions may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability or to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize or purify polypeptides. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobin molecules together with another protein or part thereof. In drug discovery, for example, proteins have been fused with antibody Fc portions for the purpose of high-throughout screening assays to identify antagonists. See for example, {Bennett, D. et al., 1995} and {Johanson, K. et al., 1995}.

The *S. pneumoniae* hyperimmune serum reactive antigen or a fragment thereof can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, hydroxylapatite chromatography and lectin chromatography.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention can be produced by chemical synthesis as well as by biotechnological means. The latter comprise the transfection or transformation of a host cell with a vector containing a nucleic acid according to the present invention and the cultivation of the transfected or transformed host cell under conditions, which are known to the ones skilled in the art. The production method may also comprise a purification step in order to purify or isolate the polypeptide to be manufactured. In a preferred embodiment the vector is a vector according to the present invention.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used for the detection of the organism or organisms in a sample containing these organisms or polypeptides derived thereof. Preferably such detection is for diagnosis, more preferable for the diagnosis

of a disease, most preferably for the diagnosis of a diseases related or linked to the presence or abundance of Gram-positive bacteria, especially bacteria selected from the group comprising streptococci, staphylococci and lactococci. More preferably, the microorganisms are selected from the group comprising *Streptococcus agalactiae*, *Streptococcus pyogenes* and *Streptococcus mutans*, especially the microorganism is *Streptococcus pyogenes*.

The present invention also relates to diagnostic assays such as quantitative and diagnostic assays for detecting levels of the hyperimmune serum reactive antigens and fragments thereof of the present invention in cells and tissues, including determination of normal and abnormal levels. Thus, for instance, a diagnostic assay in accordance with the invention for detecting over-expression of the polypeptide compared to normal control tissue samples may be used to detect the presence of an infection, for example, and to identify the infecting organism. Assay techniques that can be used to determine levels of a polypeptide, in a sample derived from a host are well known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays. Among these, ELISAs frequently are preferred. An ELISA assay initially comprises preparing an antibody specific to the polypeptide, preferably a monoclonal antibody. In addition, a reporter antibody generally is prepared which binds to the monoclonal antibody. The reporter antibody is attached to a detectable reagent such as radioactive, fluorescent or enzymatic reagent, such as horseradish peroxidase enzyme.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may also be used for the purpose of or in connection with an array. More particularly, at least one of the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be immobilized on a support. Said support typically comprises a variety of hyperimmune serum reactive antigens and fragments thereof whereby the variety may be created by using one or several of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and/or hyperimmune serum reactive antigens and fragments thereof being different. The characterizing feature of such array as well as of any array in general is the fact that at a distinct or predefined region or position on said support or a surface thereof, a distinct polypeptide is immobilized. Because of this any activity at a distinct position or region of an array can be correlated with a specific polypeptide. The number of different hyperimmune serum reactive antigens and fragments thereof immobilized on a support may range from as little as 10 to several 1000 different hyperimmune serum reactive antigens and fragments thereof. The density of hyperimmune serum reactive antigens and fragments thereof per cm^2 is in a preferred embodiment as little as 10 peptides/polypeptides per cm^2 to at least 400 different peptides/polypeptides per cm^2 and more particularly at least 1000 different hyperimmune serum reactive antigens and fragments thereof per cm^2.

The manufacture of such arrays is known to the one skilled in the art and, for example, described in US patent 5,744,309. The array preferably comprises a planar, porous or non-porous solid support having at least a first surface. The hyperimmune serum reactive antigens and fragments thereof as disclosed herein, are immobilized on said surface. Preferred support materials are, among others, glass or cellulose. It is also within the present invention that the array is used for any of the diagnostic applications described herein. Apart from the hyperimmune serum reactive antigens and fragments thereof according to the present invention also the nucleic acid molecules according to the present invention may be used for the generation of an array as described above. This applies as well to an array made of antibodies, preferably monoclonal antibodies as, among others, described herein.

In a further aspect the present invention relates to an antibody directed to any of the hyperimmune serum reactive antigens and fragments thereof, derivatives or fragments thereof according to the present invention. The present invention includes, for example, monoclonal and polyclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of a Fab expression

library. It is within the present invention that the antibody may be chimeric, i. e. that different parts thereof stem from different species or at least the respective sequences are taken from different species.

Antibodies generated against the hyperimmune serum reactive antigens and fragments thereof corresponding to a sequence of the present invention can be obtained by direct injection of the hyperimmune serum reactive antigens and fragments thereof into an animal or by administering the hyperimmune serum reactive antigens and fragments thereof to an animal, preferably a non-human. The antibody so obtained will then bind the hyperimmune serum reactive antigens and fragments thereof itself. In this manner, even a sequence encoding only a fragment of a hyperimmune serum reactive antigen and fragments thereof can be used to generate antibodies binding the whole native hyperimmune serum reactive antigen and fragments thereof. Such antibodies can then be used to isolate the hyperimmune serum reactive antigens and fragments thereof from tissue expressing those hyperimmune serum reactive antigens and fragments thereof.

For preparation of monoclonal antibodies, any technique known in the art, which provides antibodies produced by continuous cell line cultures can be used (as described originally in {Kohler, G. et al., 1975}.

Techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to immunogenic hyperimmune serum reactive antigens and fragments thereof according to this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies to immunogenic hyperimmune serum reactive antigens and fragments thereof according to this invention.

Alternatively, phage display technology or ribosomal display could be utilized to select antibody genes with binding activities towards the hyperimmune serum reactive antigens and fragments thereof either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing respective target antigens or from naïve libraries {McCafferty, J. et al., 1990}; {Marks, J. et al., 1992}. The affinity of these antibodies can also be improved by chain shuffling {Clackson, T. et al., 1991}.

If two antigen binding domains are present, each domain may be directed against a different epitope – termed 'bispecific' antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the hyperimmune serum reactive antigens and fragments thereof or purify the hyperimmune serum reactive antigens and fragments thereof of the present invention by attachment of the antibody to a solid support for isolation and/or purification by affinity chromatography.

Thus, among others, antibodies against the hyperimmune serum reactive antigens and fragments thereof of the present invention may be employed to inhibit and/or treat infections, particularly bacterial infections and especially infections arising from *S. pneumoniae*.

Hyperimmune serum reactive antigens and fragments thereof include antigenically, epitopically or immunologically equivalent derivatives, which form a particular aspect of this invention. The term "antigenically equivalent derivative" as used herein encompasses a hyperimmune serum reactive antigen and fragments thereof or its equivalent which will be specifically recognized by certain antibodies which, when raised to the protein or hyperimmune serum reactive antigen and fragments thereof according to the present invention, interfere with the interaction between pathogen and mammalian host. The term "immunologically equivalent derivative" as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

The hyperimmune serum reactive antigens and fragments thereof, such as an antigenically or

immunologically equivalent derivative or a fusion protein thereof can be used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the hyperimmune serum reactive antigens and fragments thereof. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein, for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively, an antigenic peptide comprising multiple copies of the protein or hyperimmune serum reactive antigen and fragments thereof, or an antigenically or immunologically equivalent hyperimmune serum reactive antigen and fragments thereof, may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

Preferably the antibody or derivative thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized", wherein the complimentarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in {Jones, P. et al., 1986} or {Tempest, P. et al., 1991}.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscle, delivery of DNA complexed with specific protein carriers, coprecipitation of DNA with calcium phosphate, encapsulation of DNA in various forms of liposomes, particle bombardment {Tang, D. et al., 1992}; {Eisenbraun, M. et al., 1993} and *in vivo* infection using cloned retroviral vectors {Seeger, C. et al., 1984}.

In a further aspect the present invention relates to a peptide binding to any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such peptides whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and the basic steps are known to the one skilled in the art.

Such peptides may be generated by using methods according to the state of the art such as phage display or ribosome display. In case of phage display, basically a library of peptides is generated, in form of phages, and this kind of library is contacted with the target molecule, in the present case a hyperimmune serum reactive antigen and fragments thereof according to the present invention. Those peptides binding to the target molecule are subsequently removed, preferably as a complex with the target molecule, from the respective reaction. It is known to the one skilled in the art that the binding characteristics, at least to a certain extent, depend on the particularly realized experimental set-up such as the salt concentration and the like. After separating those peptides binding to the target molecule with a higher affinity or a bigger force, from the non-binding members of the library, and optionally also after removal of the target molecule from the complex of target molecule and peptide, the respective peptide(s) may subsequently be characterised. Prior to the characterisation optionally an amplification step is realized such as, e. g. by propagating the peptide encoding phages. The characterisation preferably comprises the sequencing of the target binding peptides. Basically, the peptides are not limited in their lengths, however, preferably peptides having a lengths from about 8 to 20 amino acids are preferably obtained in the respective methods. The size of the libraries may be about 10^2 to 10^{18}, preferably 10^8 to 10^{15} different peptides, however, is not limited thereto.

A particular form of target binding hyperimmune serum reactive antigens and fragments thereof are the so-called "anticalines" which are, among others, described in German patent application DE 197 42 706.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such functional nucleic acids whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are

preferably aptamers and spiegelmers.

Aptamers are D-nucleic acids, which are either single stranded or double stranded and which specifically interact with a target molecule. The manufacture or selection of aptamers is, e.g. described in European patent EP 0 533 838. Basically the following steps are realized. First, a mixture of nucleic acids, i. e. potential aptamers, is provided whereby each nucleic acid typically comprises a segment of several, preferably at least eight subsequent randomised nucleotides. This mixture is subsequently contacted with the target molecule whereby the nucleic acid(s) bind to the target molecule, such as based on an increased affinity towards the target or with a bigger force thereto, compared to the candidate mixture. The binding nucleic acid(s) are/is subsequently separated from the remainder of the mixture. Optionally, the thus obtained nucleic acid(s) is amplified using, e.g. polymerase chain reaction. These steps may be repeated several times giving at the end a mixture having an increased ratio of nucleic acids specifically binding to the target from which the final binding nucleic acid is then optionally selected. These specifically binding nucleic acid(s) are referred to as aptamers. It is obvious that at any stage of the method for the generation or identification of the aptamers samples of the mixture of individual nucleic acids may be taken to determine the sequence thereof using standard techniques. It is within the present invention that the aptamers may be stabilized such as, e. g., by introducing defined chemical groups which are known to the one skilled in the art of generating aptamers. Such modification may for example reside in the introduction of an amino group at the 2'-position of the sugar moiety of the nucleotides. Aptamers are currently used as therapeutical agents. However, it is also within the present invention that the thus selected or generated aptamers may be used for target validation and/or as lead substance for the development of medicaments, preferably of medicaments based on small molecules. This is actually done by a competition assay whereby the specific interaction between the target molecule and the aptamer is inhibited by a candidate drug whereby upon replacement of the aptamer from the complex of target and aptamer it may be assumed that the respective drug candidate allows a specific inhibition of the interaction between target and aptamer, and if the interaction is specific, said candidate drug will, at least in principle, be suitable to block the target and thus decrease its biological availability or activity in a respective system comprising such target. The thus obtained small molecule may then be subject to further derivatisation and modification to optimise its physical, chemical, biological and/or medical characteristics such as toxicity, specificity, biodegradability and bioavailability.

Spiegelmers and their generation or manufacture is based on a similar principle. The manufacture of spiegelmers is described in international patent application WO 98/08856. Spiegelmers are L-nucleic acids, which means that they are composed of L-nucleotides rather than D-nucleotides as aptamers are. Spiegelmers are characterized by the fact that they have a very high stability in biological systems and, comparable to aptamers, specifically interact with the target molecule against which they are directed. In the process of generating spiegelmers, a heterogeonous population of D-nucleic acids is created and this population is contacted with the optical antipode of the target molecule, in the present case for example with the D-enantiomer of the naturally occurring L-enantiomer of the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Subsequently, those D-nucleic acids are separated which do not interact with the optical antipode of the target molecule. But those D-nucleic acids interacting with the optical antipode of the target molecule are separated, optionally identified and/or sequenced and subsequently the corresponding L-nucleic acids are synthesized based on the nucleic acid sequence information obtained from the D-nucleic acids. These L-nucleic acids which are identical in terms of sequence with the aforementioned D-nucleic acids interacting with the optical antipode of the target molecule, will specifically interact with the naturally occurring target molecule rather than with the optical antipode thereof. Similar to the method for the generation of aptamers it is also possible to repeat the various steps several times and thus to enrich those nucleic acids specifically interacting with the optical antipode of the target molecule.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the nucleic acid molecules according to the present invention, and a method for the manufacture of such

functional nucleic acids whereby the method is characterized by the use of the nucleic acid molecules and their respective sequences according to the present invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are preferably ribozymes, antisense oligonucleotides and siRNA.

Ribozymes are catalytically active nucleic acids which preferably consist of RNA which basically comprises two moieties. The first moiety shows a catalytic activity whereas the second moiety is responsible for the specific interaction with the target nucleic acid, in the present case the nucleic acid coding for the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Upon interaction between the target nucleic acid and the second moiety of the ribozyme, typically by hybridisation and Watson-Crick base pairing of essentially complementary stretches of bases on the two hybridising strands, the catalytically active moiety may become active which means that it catalyses, either intramolecularly or intermolecularly, the target nucleic acid in case the catalytic activity of the ribozyme is a phosphodiesterase activity. Subsequently, there may be a further degradation of the target nucleic acid, which in the end results in the degradation of the target nucleic acid as well as the protein derived from the said target nucleic acid. Ribozymes, their use and design principles are known to the one skilled in the art, and, for example described in (Doherty, E. et al., 2001) and (Lewin, A. et al., 2001).

The activity and design of antisense oligonucleotides for the manufacture of a medicament and as a diagnostic agent, respectively, is based on a similar mode of action. Basically, antisense oligonucleotides hybridise based on base complementarity, with a target RNA, preferably with a mRNA, thereby activating RNase H. RNase H is activated by both phosphodiester and phosphorothioate-coupled DNA. Phosphodiester-coupled DNA, however, is rapidly degraded by cellular nucleases with the exception of phosphorothioate-coupled DNA. These resistant, non-naturally occurring DNA derivatives do not inhibit RNase H upon hybridisation with RNA. In other words, antisense polynucleotides are only effective as DNA RNA hybride complexes. Examples for this kind of antisense oligonucleotides are described, among others, in US-patent US 5,849,902 and US 5,989,912. In other words, based on the nucleic acid sequence of the target molecule which in the present case are the nucleic acid molecules for the hyperimmune serum reactive antigens and fragments thereof according to the present invention, either from the target protein from which a respective nucleic acid sequence may in principle be deduced, or by knowing the nucleic acid sequence as such, particularly the mRNA, suitable antisense oligonucleotides may be designed base on the principle of base complementarity.

Particularly preferred are antisense-oligonucleotides, which have a short stretch of phosphorothioate DNA (3 to 9 bases). A minimum of 3 DNA bases is required for activation of bacterial RNase H and a minimum of 5 bases is required for mammalian RNase H activation. In these chimeric oligonucleotides there is a central region that forms a substrate for RNase H that is flanked by hybridising "arms" comprised of modified nucleotides that do not form substrates for RNase H. The hybridising arms of the chimeric oligonucleotides may be modified such as by 2'-O-methyl or 2'-fluoro. Alternative approaches used methylphosphonate or phosphoramidate linkages in said arms. Further embodiments of the antisense oligonucleotide useful in the practice of the present invention are P-methoxyoligonucleotides, partial P-methoxyoligodeoxyribonucleotides or P-methoxyoligonucleotides.

Of particular relevance and usefulness for the present invention are those antisense oligonucleotides as more particularly described in the above two mentioned US patents. These oligonucleotides contain no naturally occurring 5'→3'-linked nucleotides. Rather the oligonucleotides have two types of nucleotides: 2'-deoxyphosphorothioate, which activate RNase H, and 2'-modified nucleotides, which do not. The linkages between the 2'-modified nucleotides can be phosphodiesters, phosphorothioate or P-ethoxyphosphodiester. Activation of RNase H is accomplished by a contiguous RNase H-activating region, which contains between 3 and 5 2'-deoxyphosphorothioate nucleotides to activate bacterial RNase H and between 5 and 10 2'- deoxyphosphorothioate nucleotides to activate eucaryotic and, particularly,

mammalian RNase H. Protection from degradation is accomplished by making the 5′ and 3′ terminal bases highly nuclease resistant and, optionally, by placing a 3′ terminal blocking group.

More particularly, the antisense oligonucleotide comprises a 5′ terminus and a 3′ terminus; and from position 11 to 59 5′→3′-linked nucleotides independently selected from the group consisting of 2′-modified phosphodiester nucleotides and 2′-modified P-alkyloxyphosphotriester nucleotides; and wherein the 5′-terminal nucleoside is attached to an RNase H-activating region of between three and ten contiguous phosphorothioate-linked deoxyribonucleotides, and wherein the 3′-terminus of said oligonucleotide is selected from the group consisting of an inverted deoxyribonucleotide, a contiguous stretch of one to three phosphorothioate 2′-modified ribonucleotides, a biotin group and a P-alkyloxyphosphotriester nucleotide.

Also an antisense oligonucleotide may be used wherein not the 5′ terminal nucleoside is attached to an RNase H-activating region but the 3′ terminal nucleoside as specified above. Also, the 5′ terminus is selected from the particular group rather than the 3′ terminus of said oligonucleotide.

The nucleic acids as well as the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used as or for the manufacture of pharmaceutical compositions, especially vaccines. Preferably such pharmaceutical composition, preferably vaccine is for the prevention or treatment of diseases caused by, related to or associated with S. *pneumoniae*. In so far another aspect of the invention relates to a method for inducing an immunological response in an individual, particularly a mammal, which comprises inoculating the individual with the hyperimmune serum reactive antigens and fragments thereof of the invention, or a fragment or variant thereof, adequate to produce antibodies to protect said individual from infection, particularly *streptococcal* infection and most particularly *S. pneumoniae* infections.

Yet another aspect of the invention relates to a method of inducing an immunological response in an individual which comprises, through gene therapy or otherwise, delivering a nucleic acid functionally encoding hyperimmune serum reactive antigens and fragments thereof, or a fragment or a variant thereof, for expressing the hyperimmune serum reactive antigens and fragments thereof, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibodies or a cell mediated T cell response, either cytokine-producing T cells or cytotoxic T cells, to protect said individual from disease, whether that disease is already established within the individual or not. One way of administering the gene is by accelerating it into the desired cells as a coating on particles or otherwise.

A further aspect of the invention relates to an immunological composition which, when introduced into a host capable of having induced within it an immunological response, induces an immunological response in such host, wherein the composition comprises recombinant DNA which codes for and expresses an antigen of the hyperimmune serum reactive antigens and fragments thereof of the present invention. The immunological response may be used therapeutically or prophylactically and may take the form of antibody immunity or cellular immunity such as that arising from CTL or CD4+ T cells.

The hyperimmune serum reactive antigens and fragments thereof of the invention or a fragment thereof may be fused with a co-protein which may not by itself produce antibodies, but is capable of stabilizing the first protein and producing a fused protein which will have immunogenic and protective properties. This fused recombinant protein preferably further comprises an antigenic co-protein, such as Glutathione-S-transferase (GST) or beta-galactosidase, relatively large co-proteins which solubilise the protein and facilitate production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system. The co-protein may be attached to either the amino or carboxy terminus of the first protein.

Also, provided by this invention are methods using the described nucleic acid molecule or particular

fragments thereof in such genetic immunization experiments in animal models of infection with *S. pneumoniae*. Such fragments will be particularly useful for identifying protein epitopes able to provoke a prophylactic or therapeutic immune response. This approach can allow for the subsequent preparation of monoclonal antibodies of particular value from the requisite organ of the animal successfully resisting or clearing infection for the development of prophylactic agents or therapeutic treatments of *S. pneumoniae* infection in mammals, particularly humans.

The hyperimmune serum reactive antigens and fragments thereof may be used as an antigen for vaccination of a host to produce specific antibodies which protect against invasion of bacteria, for example by blocking adherence of bacteria to damaged tissue. Examples of tissue damage include wounds in skin or connective tissue and mucosal tissues caused e.g. by viral infection (esp. respiratory, such as the flu) mechanical, chemical or thermal damage or by implantation of indwelling devices, or wounds in the mucous membranes, such as the mouth, mammary glands, urethra or vagina.

The present invention also includes a vaccine formulation, which comprises the immunogenic recombinant protein together with a suitable carrier. Since the protein may be broken down in the stomach, it is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, intradermal intranasal or tramsdermal. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials, and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in-water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

According to another aspect, the present invention relates to a pharmaceutical composition comprising such a hyperimmune serum-reactive antigen or a fragment thereof as provided in the present invention for *S. pneumoniae*. Such a pharmaceutical composition may comprise one or more hyperimmune serum reactive antigens or fragments thereof against *S. pneumoniae*. Optionally, such *S. pneumoniae* hyperimmune serum reactive antigens or fragments thereof may also be combined with antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *S. pneumoniae* and/or other pathogens against which the antigens have been included in the vaccine.

According to a further aspect, the present invention relates to a pharmaceutical composition comprising a nucleic acid molecule encoding a hyperimmune serum-reactive antigen or a fragment thereof as identified above for *S. pneumoniae*. Such a pharmaceutical composition may comprise one or more nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof against *S. pneumoniae*. Optionally, such *S. pneumoniae* nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof may also be combined with nucleic acid molecules encoding antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *S. pneumoniae* and/or other pathogens against which the antigens have been included in the vaccine.

The pharmaceutical composition may contain any suitable auxiliary substances, such as buffer substances, stabilisers or further active ingredients, especially ingredients known in connection of pharmaceutical composition and/or vaccine production.

A preferable carrier/or excipient for the hyperimmune serum-reactive antigens, fragments thereof or a

coding nucleic acid molecule thereof according to the present invention is an immunostimulatory compound for further stimulating the immune response to the given hyperimmune serum-reactive antigen, fragment thereof or a coding nucleic acid molecule thereof. Preferably the immunostimulatory compound in the pharmaceutical preparation according to the present invention is selected from the group of polycationic substances, especially polycationic peptides, immunostimulatory nucleic acids molecules, preferably immunostimulatory deoxynucleotides, alum, Freund's complete adjuvants, Freund's incomplete adjuvants, neuroactive compounds, especially human growth hormone, or combinations thereof.

It is also within the scope of the present invention that the pharmaceutical composition, especially vaccine, comprises apart from the hyperimmune serum reactive antigens, fragments thereof and/or coding nucleic acid molecules thereof according to the present invention other compounds which are biologically or pharmaceutically active. Preferably, the vaccine composition comprises at least one polycationic peptide. The polycationic compound(s) to be used according to the present invention may be any polycationic compound, which shows the characteristic effects according to the WO 97/30721. Preferred polycationic compounds are selected from basic polyppetides, organic polycations, basic polyamino acids or mixtures thereof. These polyamino acids should have a chain length of at least 4 amino acid residues (WO 97/30721). Especially preferred are substances like polylysine, polyarginine and polypeptides containing more than 20 %, especially more than 50 % of basic amino acids in a range of more than 8, especially more than 20, amino acid residues or mixtures thereof. Other preferred polycations and their pharmaceutical compositions are described in WO 97/30721 (e.g. polyethyleneimine) and WO 99/38528. Preferably these polypeptides contain between 20 and 500 amino acid residues, especially between 30 and 200 residues.

These polycationic compounds may be produced chemically or recombinantly or may be derived from natural sources.

Cationic (poly)peptides may also be anti-microbial with properties as reviewed in {Ganz, T., 1999}. These (poly)peptides may be of prokaryotic or animal or plant origin or may be produced chemically or recombinantly (WO 02/13857). Peptides may also belong to the class of defensins (WO 02/13857). Sequences of such peptides can be, for example, found in the Antimicrobial Sequences Database under the following internet address:

http://www.bbcm.univ.trieste.it/~tossi/pag2.html

Such host defence peptides or defensives are also a preferred form of the polycationic polymer according to the present invention. Generally, a compound allowing as an end product activation (or down-regulation) of the adaptive immune system, preferably mediated by APCs (including dendritic cells) is used as polycationic polymer.

Especially preferred for use as polycationic substances in the present invention are cathelicidin derived antimicrobial peptides or derivatives thereof (International patent application WO 02/13857, incorporated herein by reference), especially antimicrobial peptides derived from mammalian cathelicidin, preferably from human, bovine or mouse.

Polycationic compounds derived from natural sources include HIV-REV or HIV-TAT (derived cationic peptides, antennapedia peptides, chitosan or other derivatives of chitin) or other peptides derived from these peptides or proteins by biochemical or recombinant production. Other preferred polycationic compounds are cathelin or related or derived substances from cathelin. For example, mouse cathelin is a peptide which has the amino acid sequence NH_2-RLAGLLRKGGEKIGEKLKKIGOKIKNFFQKLVPQPE-COOH. Related or derived cathelin substances contain the whole or parts of the cathelin sequence with at least 15-20 amino acid residues. Derivations may include the substitution or modification of the natural

amino acids by amino acids which are not among the 20 standard amino acids. Moreover, further cationic residues may be introduced into such cathelin molecules. These cathelin molecules are preferred to be combined with the antigen. These cathelin molecules surprisingly have turned out to be also effective as an adjuvant for an antigen without the addition of further adjuvants. It is therefore possible to use such cathelin molecules as efficient adjuvants in vaccine formulations with or without further immunactivating substances.

Another preferred polycationic substance to be used according to the present invention is a synthetic peptide containing at least 2 KLK-motifs separated by a linker of 3 to 7 hydrophobic amino acids (International patent application WO 02/32451, incorporated herein by reference).

The pharmaceutical composition of the present invention may further comprise immunostimulatory nucleic acid(s). Immunostimulatory nucleic acids are e. g. neutral or artificial CpG containing nucleic acids, short stretches of nucleic acids derived from non-vertebrates or in form of short oligonucleotides (ODNs) containing non-methylated cytosine-guanine di-nucleotides (CpG) in a certain base context (e.g. described in WO 96/02555). Alternatively, also nucleic acids based on inosine and cytidine as e.g. described in the WO 01/93903, or deoxynucleic acids containing deoxy-inosine and/or deoxyuridine residues (described in WO 01/93905 and PCT/EP 02/05448, incorporated herein by reference) may preferably be used as immunostimulatory nucleic acids for the present invention. Preferablly, the mixtures of different immunostimulatory nucleic acids may be used according to the present invention.

It is also within the present invention that any of the aforementioned polycationic compounds is combined with any of the immunostimulatory nucleic acids as aforementioned. Preferably, such combinations are according to the ones as described in WO 01/93905, WO 02/32451, WO 01/54720, WO 01/93903, WO 02/13857 and PCT/EP 02/05448 and the Austrian patent application A 1924/2001, incorporated herein by reference.

In addition or alternatively such vaccine composition may comprise apart from the hyperimmune serum reactive antigens and fragments thereof, and the coding nucleic acid molecules thereof according to the present invention a neuroactive compound. Preferably, the neuroactive compound is human growth factor as, e.g. described in WO 01/24822. Also preferably, the neuroactive compound is combined with any of the polycationic compounds and/or immunostimulatory nucleic acids as afore-mentioned.

In a further aspect the present invention is related to a pharmaceutical composition. Such pharmaceutical composition is, for example, the vaccine described herein. Also a pharmaceutical composition is a pharmaceutical composition which comprises any of the following compounds or combinations thereof: the nucleic acid molecules according to the present invention, the hyperimmune serum reactive antigens and fragments thereof according to the present invention, the vector according to the present invention, the cells according to the present invention, the antibody according to the present invention, the functional nucleic acids according to the present invention and the binding peptides such as the anticalines according to the present invention, any agonists and antagonists screened as described herein. In connection therewith any of these compounds may be employed in combination with a non-sterile or sterile carrier or carriers for use with cells, tissues or organisms, such as a pharmaceutical carrier suitable for administration to a subject. Such compositions comprise, for instance, a media additive or a therapeutically effective amount of a hyperimmune serum reactive antigen and fragments thereof of the invention and a pharmaceutically acceptable carrier or excipient. Such carriers may include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. The formulation should suit the mode of administration.

The pharmaceutical compositions may be administered in any effective, convenient manner including, for instance, administration by topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intratracheal or intradermal routes among others.

In therapy or as a prophylactic, the active agent may be administered to an individual as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application, for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol or oleyl alcohol for lotions. Such carriers may constitute from about 1 % to about 98 % by weight of the formulation; more usually they will constitute up to about 80 % by weight of the formulation.

In addition to the therapy described above, the compositions of this invention may be used generally as a wound treatment agent to prevent adhesion of bacteria to matrix proteins exposed in wound tissue and for prophylactic use in dental treatment as an alternative to, or in conjunction with, antibiotic prophylaxis.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response. A suitable unit dose for vaccination is 0.05-5 μg antigen / per kg of body weight, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

With the indicated dose range, no adverse toxicological effects should be observed with the compounds of the invention, which would preclude their administration to suitable individuals.

In a further embodiment the present invention relates to diagnostic and pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. The ingredient(s) can be present in a useful amount, dosage, formulation or combination. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, reflecting approval by the agency of the manufacture, use or sale of the product for human administration.

In connection with the present invention any disease related use as disclosed herein such as, e. g. use of the pharmaceutical composition or vaccine, is particularly a disease or diseased condition which is caused by, linked or associated with Streptococci, more preferably, *S. pneumoniae*. In connection therewith it is to be noted that *S. pneumoniae* comprises several strains including those disclosed herein. A disease related, caused or associated with the bacterial infection to be prevented and/or treated according to the present invention includes besides others bacterial pharyngitis, otitis media, pneumonia, bacteremia, meningitis, peritonitis and sepsis in humans.

In a still further embodiment the present invention is related to a screening method using any of the hyperimmune serum reactive antigens or nucleic acids according to the present invention. Screening methods as such are known to the one skilled in the art and can be designed such that an agonist or an antagonist is screened. Preferably an antagonist is screened which in the present case inhibits or prevents the binding of any hyperimmune serum reactive antigen and fragment thereof according to the present invention to an interaction partner. Such interaction partner can be a naturally occurring interaction partner or a non-naturally occurring interaction partner.

The invention also provides a method of screening compounds to identify those, which enhance (agonist) or block (antagonist) the function of hyperimmune serum reactive antigens and fragments thereof or nucleic acid molecules of the present invention, such as its interaction with a binding molecule. The

method of screening may involve high-throughput.

For example, to screen for agonists or antagonists, the interaction partner of the nucleic acid molecule and nucleic acid, respectively, according to the present invention, maybe a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, may be prepared from a cell that expresses a molecule that binds to the hyperimmune serum reactive antigens and fragments thereof of the present invention. The preparation is incubated with labelled hyperimmune serum reactive antigens and fragments thereof in the absence or the presence of a candidate molecule, which may be an agonist or antagonist. The ability of the candidate molecule to bind the binding molecule is reflected in decreased binding of the labelled ligand. Molecules which bind gratuitously, i. e., without inducing the functional effects of the hyperimmune serum reactive antigens and fragments thereof, are most likely to be good antagonists. Molecules that bind well and elicit functional effects that are the same as or closely related to the hyperimmune serum reactive antigens and fragments thereof are good agonists.

The functional effects of potential agonists and antagonists may be measured, for instance, by determining the activity of a reporter system following interaction of the candidate molecule with a cell or appropriate cell preparation, and comparing the effect with that of the hyperimmune serum reactive antigens and fragments thereof of the present invention or molecules that elicit the same effects as the hyperimmune serum reactive antigens and fragments thereof. Reporter systems that may be useful in this regard include but are not limited to colorimetric labelled substrate converted into product, a reporter gene that is responsive to changes in the functional activity of the hyperimmune serum reactive antigens and fragments thereof, and binding assays known in the art.

Another example of an assay for antagonists is a competitive assay that combines the hyperimmune serum reactive antigens and fragments thereof of the present invention and a potential antagonist with membrane-bound binding molecules, recombinant binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. The hyperimmune serum reactive antigens and fragments thereof can be labelled such as by radioactivity or a colorimetric compound, such that the molecule number of hyperimmune serum reactive antigens and fragments thereof bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a hyperimmune serum reactive antigen and fragments thereof of the invention and thereby inhibit or extinguish its acitivity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds to the same sites on a binding molecule without inducing functional activity of the hyperimmune serum reactive antigens and fragments thereof of the invention.

Potential antagonists include a small molecule, which binds to and occupies the binding site of the hyperimmune serum reactive antigens and fragments thereof thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules.

Other potential antagonists include antisense molecules (see {Okano, H. et al., 1991}; OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION; CRC Press, Boca Ration, FL (1988), for a description of these molecules).

Preferred potential antagonists include derivatives of the hyperimmune serum reactive antigens and fragments thereof of the invention.

As used herein the activity of a hyperimmune serum reactive antigen and fragment thereof according to the present invention is its capability to bind to any of its interaction partner or the extent of such capability to bind to its or any interaction partner.

In a particular aspect, the invention provides the use of the hyperimmune serum reactive antigens and fragments thereof, nucleic acid molecules or inhibitors of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: i) in the prevention of adhesion of *S. pneumoniae* to mammalian extracellular matrix proteins at mucosal surfaces and on in-dwelling devices or to extracellular matrix proteins in wounds; ii) to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins which mediate tissue damage or invasion iii) or lead to evasion of immune defense; iv) to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques, e.g. through inhibiting nutrient acquisition {Brown, J. et al., 2001}.

Each of the DNA coding sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein upon expression can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The antagonists and agonists may be employed, for instance, to inhibit diseases arising from infection with Streptococcus, especially *S. pneumoniae*, such as sepsis.

In a still further aspect the present invention is related to an affinity device such affinity device comprises as least a support material and any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, which is attached to the support material. Because of the specificity of the hyperimmune serum reactive antigens and fragments thereof according to the present invention for their target cells or target molecules or their interaction partners, the hyperimmune serum reactive antigens and fragments thereof allow a selective removal of their interaction partner(s) from any kind of sample applied to the support material provided that the conditions for binding are met. The sample may be a biological or medical sample, including but not limited to, fermentation broth, cell debris, cell preparation, tissue preparation, organ preparation, blood, urine, lymph liquid, liquor and the like.

The hyperimmune serum reactive antigens and fragments thereof may be attached to the matrix in a covalent or non-covalent manner. Suitable support material is known to the one skilled in the art and can be selected from the group comprising cellulose, silicon, glass, aluminium, paramagnetic beads, starch and dextrane.

The present invention is further illustrated by the following figures, examples and the sequence listing, from which further features, embodiments and advantages may be taken. It is to be understood that the present examples are given by way of illustration only and not by way of limitation of the disclosure.

In connection with the present invention

Figure 1 shows the characterization of *S. pneumoniae* specific human sera.

Figure 2 shows the characterization of the small fragment genomic library, LSPn-70, from *Streptococcus pneumoniae* serotype 4.

Figure 3 shows the selection of bacterial cells by MACS using biotinylated human IgGs.

Figure 4 shows an example for the gene distribution study with the identified antigens.

Figure 5 shows examples of changes in epitope-specific antibody levels in the different age groups and during the course of pneumococcal disease.

Figure 6 shows examples for cell surface staining with epitope-specific antisera by flow cytometry.

Figure 7 shows the determination of bactericidal activity of antibodies induced by selected epitopes in an *in vitro assay.*

Table 1 shows the summary of all screens performed with genomic *S. pneumoniae* libraries and human serum.

Table 2 shows the summary of epitope serology analysis with human sera.

Table 3 shows the summary of the gene distribution analysis for the identified antigens in 50 *S. pneumoniae* strains.

Table 4 shows the summary of the surface staining and bactericidal activity measurements.

The figures to which it might be referred to in the specification are described in the following in more details.

Figure 1 shows the characterization of human sera for anti-*S. pneumoniae* antibodies ass measured by immune assays. Total anti-*S. pneumoniae* IgG and IgA antibody levels were measured by standard ELISA using total bacterial lysates or culture supernant fractions prepared from *S. pneumoniae* serotype 4 capsule negative mutant strain as coating antigens. 97 serum samples from convalescing patients with inasive diseases or 50 sera from healthy adults without nasopharyngeal carriage of *S. pneumoniae* were analysed at three different serum dilutions. Results of representative experiments are shown with **(A)** patients' sera with bacterial lysate and **(B)** healthy adult sera with culture superntant proteins. Data are expressed as ELISA units calculated from absorbance at 405nm at a serum dilution in the linear range of detection (10.000X for IgA, 50,000 for IgG). 2x5 sera from both donor groups were selected and pooled for antigen identification by bacterial surface display. Selected sera included in the two patient (PSPn3-IgG,-IgA and PSPn7-IgG) and two healthy pools (NSPn4-IgG,-IgA and NSPn5-IgG) are indicated by circules. **(C)** Immunoblot analysis was performed on sera pre-selected by ELISA in order to ensure multiple immune reactivity with protein antigens. Results of a representative experiment using total bacterial lysate prepared from *S. pneumoniae* serotype 4 capsule negative mutant strain and selected patients' sera at 5.000X dilution are shown. Not selected, low titer sera were included as negative controls. Mw: molecular weigth markers. **(D)** Surface staining of *S. pneumoniae* serotype 4 capsule negative mutant strain was performed by FACS to compare antibody binding to surface located antigens. Human sera were used at different concentrations (0.5-5%). Representative data are shown with patients' sera used at 0.5% final concentration. Signal was detected with FITC-labeled anti-human IgGFab and analysed with the computer program CELLQuest. **(E)** Correlation between IgG titers measured by ELISA using total bacterial lysates and surface staining of whole living *S. pneumoniae* with serum IgGs is shown. IgG titer is expressed as ELISA units, while surface staining is expressed as mean fluorescence of stained bacteria calculated by the computer program CELLQuest.

Figure 2 **(A)** shows the fragment size distribution of the *Streptococcus pneumoniae* type 4 small fragment genomic library, LSPn-70. After sequencing 609 randomly selected clones sequences were trimmed to eliminate vector residues and the number of clones with various genomic fragment sizes were plotted. **(B)** shows graphic illustration of the distribution of the same set of randomly sequenced clones of LSPn-70 over the *S. pneumoniae* chromosome (according to the TIGR4 genome data). Circles indicate matching

sequences to annotated ORFs and rectangles represent fully matched clones to non-coding chromosomal sequences in +/+ or +/- orientation. Diamonds position all clones with chimeric sequences. Numeric distances in base pairs are indicated over the circular genome for orientation. Partitioning of various clone sets within the library is given in numbers and percentage at the bottom of the figure.

Figure 3 (A) shows the MACS selection with biotinylated human IgGs. The LSPn-70 library in pMAL9.1 was screened with 10 μg biotinylated IgG (PSPn3-IgG, purified from human serum). As negative control, no serum was added to the library cells for screening. Number of cells selected after the 1st and 2nd elution are shown for each selection round (upper and lower panel, respectively). **(B)** shows the reactivity of specific clones (1-26) selected by bacterial surface display as analysed by immunoblot analysis with the human serum IgG pool (PSPn7-IgG, 4μg/μl) used for selection by MACS at a dilution of 1:3,000. As a loading control the same blot was also analysed with antibodies directed against the platform protein LamB at a dilution of 1:5,000 of hyperimmune rabbit serum. LB, Extract from a clone expressing LamB without foreign peptide insert.

Figure 4 (A) shows the representation of different serotypes of *S. pneumoniae* clinical isolates analysed for the gene distribution study. **(B)** shows the PCR analysis for the gene distribution of SP1604 with the respective oligonucleotides. The predicted size of the PCR fragments is 470 bp. 1-50, *S. pneumoniae* strains, clinical isolates as listed under A; -, no genomic DNA added; +, genomic DNA from *S. pneumoniae* serotype 4, which served as template for library construction.

Figure 5 shows the ELISA measurement of epitope-specific human serum IgG antibody levels during pneumococcal disease. Three serum samples were collected longitudinally from patients with invasive pneumococcal disease, before disease occurred (pre), in the acute and convalescent phases. Representative experiments are shown with two sets of sera from two different patients, (A) P1147 and (B) P1150 reacted with peptides representing the identified antigens SP0069, SP0082, SP0117, SP1175, SP1937, SP2190 and SP2216, as indicated. Biotin-labeled peptides were reacted with human serum samples at 200X and 1.000X dilutions and data are expressed as ELISA units.

Figure 6 shows the detection of specific antibody binding on the cell surface of *Streptococcus pneumoniae* by flow cytometry. In Figure 5A preimmune mouse sera and polyclonal sera raised against *S. pneumoniae* serotype 4 lysate were incubated with *S. pneumoniae* strain serotype 4 and analysed by flow cytometry. Control shows the level of non-specific binding of the secondary antibody to the surface of *S. pneumoniae* cells. The histograms in figure **5B** indicates the increased fluorescence due to specific binding of anti-SP2216, anti-SP0117, anti-SP0454 and anti-CRF1992 antibodies in comparison to the control sera against the platform protein LamB.

Figure 7 shows the bactericidal activity of epitope specific antibodies as determined in *in vitro* killing assay. The killing activity of immune sera is measured parallel with and calculated relative to the appropriate control sera. Data are expressed as percentage of killing, that is the reduction on bacterial cfu numbers as a consequence of the presence of antibodies in hyperimmune (HI) polyclonal mouse sera generated with *S. pneumoniae* lysate **(A)**, in immune sera generated with SP0117 epitopes expressed in the LamB platform protein **(B)**, and in mouse immune sera generated with SP1287 epitopes expressed in the FhuA platform protein **(C)**. The control sera represent preimmune sera (PI), sera induced with Lamb or FhuA expressing *E. coli* clones without *S. pneumonia*-derived epitopes. *S. pneumonaie* serotype 4 cells were incubated with mouse phagocytic cells for 60 min, and surviving bacteria were quantified by counting cfus after plating on blood agar.

Table 1: Immunogenic proteins identified by bacterial surface display.
A, 300bp library in fhuA with NSPn4-IgA (362), B, 300bp library in fhuA with NSPn4-IgG (832), C, 300bp library in fhuA with NSPn5-IgG (872), D, 300bp library in fhuA with PSPn3-IgA (361), E, 300bp library in fhuA with PSPn3-IgG (575), F, 300bp library in fhuA with PSPn7-IgG (795), G, 70bp library in lamB with

NSPn4-IgA (1043); H, 70bp library in lamB with NSPn4-IgG (929), I, 70bp library in lamB with NSPn5-IgG (527), K, 70bp library in lamB with PSPn3-IgA (1121), L, 70bp library in lamB with PSPn3-IgG (1242), M, 70bp library in lamB with PSPn7-IgG (514); *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC (Kolaskar, A. et al., 1990).

Table 2: Epitope serology with human sera.
Immune reactivity of individual synthetic peptides representing selected epitopes with individual human sera is shown. Extent of reactivity is pattern/grey coded; white: - (<50U), light grey: + (50-119U); dark gery: ++ (120-199U), black: +++ (200-500U) and vertically crossed: ++++ (> 500U). ELISA units (U) are calculated from OD_{405nm} readings and the serum dilution after correction for background. S stands for score, calculated as the sum of all reactivities (addition of the number of all +); P1 to P13 sera are measured to be high titer and are from patients with invasive penumococcal diseases and N1 to N10 sera are from healthy adults with high anti-*S. pneumoniae* titers. S stands for score. Which is the sum of immune reactivities: - =0; + =1; ++ =2; +++ =3 and ++++ =4. Location of synthetic peptides within the antigenic ORFs according to the genome annotation of TIGR4 strain are given in columns **from** and **to** indicating the first and last amino acid residues, respectively. Peptide names: SP0117.1-7 present in annotated ORFSP0117; ARF0408.1, potential novel ORF in alternative reading-frame of SP0408; CRF0129.1, potential novel ORF on complement of SP0129.

Table 3: Gene distribution in *S. pneumoniae* strains.
Fifty *S. pneumoniae* strains as shown in Figure 4A were tested by PCR with oligonucleotides specific for the genes encoding relevant antigens. The PCR fragment of one selected PCR fragment was sequenced in order to confirm the amplification of the correct DNA fragment. *, number of amino acid substitutions in a serotype 14 strain as compared to *S. pneumoniae* TIGR4 (serotype 4). #, alternative strain used for sequencing, because gene was not present in the serotype 14 strain.

Table 4: Surface location of antigenic epitopes and the functionality of the epitope-specific antibodies.
45 *S. pneumoniae* antigens were tested for surface localization in the way described and presented in Figure 6 by using mouse sera generated by immunization with *E. coli* clones harboring plasmids encoding the platform proteins LamB or FhuA fused to a *S. pneumoniae* peptide. Data are summarized in the column labeled **FACS**. The very same immune reagents were used in an *in vitro* killing assay, as shown in Figure 7 for the examples, and presented for all antigens tested positive by FACS in column **PK** (phagocytic killing). -: negative result, +: not consistently positive in all assays performed, ++ and +++ are consistently positive relative to control reagents.

EXAMPLES

Example 1: Characterization and selection of human sera based anti-*S. pneumoniae* antibodies, preparation of antibody screening reagents

Experimental procedures

Enzyme linked immune assay (ELISA).
ELISA plates (Maxisorb, Millipore) were coated with 5-10 μg/ml total protein diluted in coating buffer (0.1M sodium carbonate pH 9.2). Three dilutions of sera (2,000X, 10,000X, 50,000X) were made in PBS-BSA. Highly specific Horse Radish Peroxidase (HRP)-conjugated anti-human IgG or anti-human IgA secondary antibodies (Southern Biotech) were used according to the manufacturers' recommendations (dilution: 1,000x). Antigen-antibody complexes were quantified by measuring the conversion of the substrate (ABTS) to colored product based on OD_{405nm} readings by automatic ELIAS reader (TECAN SUNRISE).

Preparation of bacterial antigen extracts

Total bacterial lysate: Bacteria were grown overnight in THB (Todd-Hewitt Broth) and lysed by repeated freeze-thaw cycles: incubation on dry ice/ethanol-mixture until frozen (1 min), then thawed at 37°C (5 min): repeated 3 times. This was followed by sonication and collection of supernatant by centrifugation (3,500 rpm, 15 min, 4°C).

Culture supernatant: After removal of bacteria by centrifugation, the supernatant of overnight grown bacterial cultures was precipitated with ice-cold ethanol by mixing 1 part supernatant with 3 parts abs. ethanol and incubated overnight at -20°C. Precipitates were collected by centrifugation (2,600 g, for 15 min). Dry pellets were dissolved either in PBS for ELISA, or in urea and SDS-sample buffer for SDS-PAGE and immunoblotting. The protein concentration of samples was determined by Bradford assay.

Immunoblotting

Total bacterial lysate and culture supernatant samples were prepared from *in vitro* grown *S. pneumoniae* serotype 4 uncapsulated mutant strain. 10 to 25µg total protein/lane was separated by SDS-PAGE using the BioRad Mini-Protean 3 Cell electrophoresis system and proteins transferred to nitrocellulose membrane (ECL, Amersham Pharmacia). After overnight blocking in 5% milk, human sera were added at 2,000x dilution, and HRPO labeled anti-human IgG was used for detection.

Surface staining of bacteria

Flow cytometric analysis was carried out as follows. *S. pneumoniae* serotype 4 uncapsulated mutant strain was grown in Todd-Hewitt broth overnight until early stationary phase. Cells were collected and washed twice in Hanks Balanced Salt Solution (HBSS) and the cell density was adjusted to approximately 1 X 10^6 CFU in 100µl HBSS with 0.5% BSA based on OD600 nm readings. After incubation with human sera at 0,5 and 2% final concentration for 60 min at 4°C, unbound antibodies were washed away by centrifugation in excess HBSS, 0.5% BSA. For detection fluorescein (FITC) labeled secondary goat anti-human IgG ($F(ab')_2$ fragment specific) was incubated with the cells at 4°C for 30 min. After washing the cells, cells were fixed with 2% paraformaldehyde. Surface staining antibodies were detected using a Becton Dickinson FACScan flow cytometer and data further analyzed with the computer program CELLQuest.

Purification of antibodies for genomic screening. Five sera from both the patient and the healthy group were selected based on the overall anti-streptococcal titers for a serum pool used in the screening procedure. Antibodies against *E. coli* proteins were removed by incubating the heat-inactivated sera with whole cell *E. coli* cells (DH5alpha, transformed with pHIE11, grown under the same condition as used for bacterial surface display). Highly enriched preparations of IgGs from the pooled, depleted sera were generated by protein G affinity chromatography, according to the manufacturer's instructions (UltraLink Immobilized Protein G, Pierce). IgA antibodies were purified also by affinity chromatography using biotin-labeled anti-human IgA (Southern Biotech) immobilized on Streptavidin-agarose (GIBCO BRL). The efficiency of depletion and purification was checked by SDS-PAGE, Western blotting, ELISA and protein concentration measurements.

Results

The antibodies produced against *S. pneumoniae* by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. These molecules are essential for the identification of individual antigens in the approach as described in the present invention, which is based on the interaction of the specific anti-streptococcal antibodies and the corresponding *S. pneumoniae* peptides or proteins. To gain access to relevant antibody repertoires, human sera were collected from

I. convalescent patients with invasive *S. pneumoniae* infections, such as pneumonia, bacteraemia and meningitis. (*S. pneumoniae* was shown to be the causative agent by medical microbiological tests),

II healthy adults without carriage at the time of sampling. *S. pneumoniae* colonization and infections are common, and antibodies are present as a consequence of natural immunization from

previous encounters.

97 serum samples from patien and 50 sera from healthy adults were characterized for anti-*S. pneumoniae* antibodies by a series of immune assays. Primary characterization was done by ELISA using two different antigen preparations, such as total bacterial extract and culture supernatant proteins prepared from *S. pneumoniae* serotype 4 uncapsulated mutant strain. It is an important aspect that we analysed uncapsulated strain, since we avoided the reactivities coming from serotype specific abundant anti-capsular polysaccharide antibodies.

Recently it was reported that not only IgG, but also IgA serum antibodies can be recognized by the FcRIII receptors of PMNs and promote opsonization {Phillips-Quagliata, J. et al., 2000}; {Shibuya, A. et al., 2000}. The primary role of IgA antibodies is neutralization, mainly at the mucosal surface. The level of serum IgA reflects the quality, quantity and specificity of the dimeric secretory IgA. For that reason the serum collection was not only analyzed for anti-streptococcal IgG, but also for IgA levels. In the ELISA assays highly specific secondary reagents were used to detect antibodies from the high affinity types, such as IgG and IgA, but avoided IgM. Production of IgM antibodies occurs during the primary adaptive humoral response, and results in low affinity antibodies, while IgG and IgA antibodies had already undergone affinity maturation, and are more valuable in fighting or preventing disease. Antibody titers were compared at given dilutions where the response was linear (Fig. 1A and 1B.). Sera were ranked based on the IgG and IgA reactivity against the two complex antigenic mixtures, and the highest ones were selected for further testing by immunoblotting. This analysis confirmed a high antibody reactivity of the pre-selected sera against multiple pneumococcal proteins, especially when compared to not selected, low-titer sera (Fig 1C). ELISA ranking of sera also correlated very well with surface staining of the same *S. pneumoniae* strain (Fig. 1D and 1E) suggesting that the majority of the antibodies detected by ELISA corresponded to surface antigens. This extensive antibody characterization approach has led to the unambiguous identification of anti-pneumococcal hyperimmune sera.

Selected sera, 2x5 from both the patient and healthy donor groups were pooled to further enrich for abundant antibodies, but still having a representation of antibody repertoires of different individuals. IgG and IgA antibodies were purified from pooled sera by affinity chromatography and depleted of E. coli -reactive antibodies to avoid background in the bacterial surface display screen.

Example 2: Generation of highly random, frame-selected, small-fragment, genomic DNA libraries of *Streptococcus pneumoniae*

Experimental procedures

Preparation of streptococcal genomic DNA. 50 ml Todd-Hewitt Broth medium was inoculated with *S. pneumoniae* serotype 4 (clinical isolate, typed with conventional serotyping) bacteria from a frozen stab and grown with aeration and shaking for 18 h at 37°C. The culture was then harvested, centrifuged with 1,600x g for 15 min and the supernatant was removed. Bacterial pellets were washed 3 x with PBS and carefully re-suspended in 0.5 ml of Lysozyme solution (100 mg/ml). 0.1 ml of 10 mg/ml heat treated RNase A and 20 U of RNase T1 were added, mixed carefully and the solution was incubated for 1 h at 37°C. Following the addition of 0.2 ml of 20 % SDS solution and 0.1 ml of Proteinase K (10 mg/ml) the tube was incubated overnight at 55°C. 1/3 volume of saturated NaCl was then added and the solution was incubated for 20 min at 4°C. The extract was pelleted in a microfuge (13,000 rpm) and the supernatant transferred into a new tube. The solution was extracted with PhOH/$CHCl_3$/IAA (25:24:1) and with $CHCl_3$/IAA (24:1). DNA was precipitated at room temperature by adding 0.6x volume of Isopropanol, spooled from the solution with a sterile Pasteur pipette and transferred into tubes containing 80% ice-cold ethanol. DNA was recovered by centrifuging the precipitates with 10-12,000x g, then dried on air and dissolved in ddH_2O.

Preparation of small genomic DNA fragments. Genomic DNA fragments were mechanically sheared into

fragments ranging in size between 150 and 300 bp using a cup-horn sonicator (Bandelin Sonoplus UV 2200 sonicator equipped with a BB5 cup horn, 10 sec. pulses at 100 % power output) or into fragments of size between 50 and 70 bp by mild DNase I treatment (Novagen). It was observed that sonication yielded a much tighter fragment size distribution when breaking the DNA into fragments of the 150-300 bp size range. However, despite extensive exposure of the DNA to ultrasonic wave-induced hydromechanical shearing force, subsequent decrease in fragment size could not be efficiently and reproducibly achieved. Therefore, fragments of 50 to 70 bp in size were obtained by mild DNase I treatment using Novagen's shotgun cleavage kit. A 1:20 dilution of DNase I provided with the kit was prepared and the digestion was performed in the presence of $MnCl_2$ in a 60 µl volume at 20°C for 5 min to ensure double-stranded cleavage by the enzyme. Reactions were stopped with 2 µl of 0.5 M EDTA and the fragmentation efficiency was evaluated on a 2% TAE-agarose gel. This treatment resulted in total fragmentation of genomic DNA into near 50-70 bp fragments. Fragments were then blunt-ended twice using T4 DNA Polymerase in the presence of 100 µM each of dNTPs to ensure efficient flushing of the ends. Fragments were used immediately in ligation reactions or frozen at -20°C for subsequent use.

Description of the vectors. The vector pMAL4.31 was constructed on a pASK-IBA backbone {Skerra, A., 1994} with the beta-lactamase (*bla*) gene exchanged with the Kanamycin resistance gene. In addition the *bla* gene was cloned into the multiple cloning site. The sequence encoding mature beta-lactamase is preceded by the leader peptide sequence of *ompA* to allow efficient secretion across the cytoplasmic membrane. Furthermore a sequence encoding the first 12 amino acids (spacer sequence) of mature beta-lactamase follows the *ompA* leader peptide sequence to avoid fusion of sequences immediately after the leader peptidase cleavage site, since e.g. clusters of positive charged amino acids in this region would decrease or abolish translocation across the cytoplasmic membrane {Kajava, A. et al., 2000}. A *Sma*I restriction site serves for library insertion. An upstream FseI site and a downstream NotI site, which were used for recovery of the selected fragment, flank the *Sma*I site. The three restriction sites are inserted after the sequence encoding the 12 amino acid spacer sequence in such a way that the *bla* gene is transcribed in the -1 reading frame resulting in a stop codon 15 bp after the *Not*I site. A +1 bp insertion restores the *bla* ORF so that beta-lactamase protein is produced with a consequent gain of Ampicillin resistance.

The vector pMAL9.1 was constructed by cloning the *lamB* gene into the multiple cloning site of pEH1 {Hashemzadeh-Bonehi, L. et al., 1998}. Subsequently, a sequence was inserted in *lamB* after amino acid 154, containing the restriction sites *Fse*I, *Sma*I and *Not*I. The reading frame for this insertion was constructed in such a way that transfer of frame-selected DNA fragments excised by digestion with *Fse*I and *Not*I from plasmid pMAL4.31 yields a continuous reading frame of *lamB* and the respective insert.

The vector pMAL10.1 was constructed by cloning the *btuB* gene into the multiple cloning site of pEH1. Subsequently, a sequence was inserted in *btuB* after amino acid 236, containing the restriction sites *Fse*I, *Xba*I and *Not*I. The reading frame for this insertion was chosen in a way that transfer of frame-selected DNA fragments excised by digestion with *Fse*I and *Not*I from plasmid pMAL4.31 yields a continuous reading frame of *btuB* and the respective insert.

The vector pHIE11 was constructed by cloning the *fhuA* gene into the multiple cloning site of pEH1. Thereafter, a sequence was inserted in *fhuA* after amino acid 405, containing the restriction site *Fse*I, *Xba*I and *Not*I. The reading frame for this insertion was chosen in a way that transfer of frame-selected DNA fragments excised by digestion with *Fse*I and *Not*I from plasmid pMAL4.31 yields a continuous reading frame of *fhuA* and the respective insert.

Cloning and evaluation of the library for frame selection. Genomic *S. pneumoniae* DNA fragments were ligated into the *Sma*I site of the vector pMAL4.31. Recombinant DNA was electroporated into DH10B electrocompetent *E. coli* cells (GIBCO BRL) and transformants plated on LB-agar supplemented with Kanamycin (50 µg/ml) and Ampicillin (50 µg/ml). Plates were incubated over night at 37°C and colonies collected for large scale DNA extraction. A representative plate was stored and saved for collecting

colonies for colony PCR analysis and large-scale sequencing. A simple colony PCR assay was used to initially determine the rough fragment size distribution as well as insertion efficiency. From sequencing data the precise fragment size was evaluated, junction intactness at the insertion site as well as the frame selection accuracy (*3n+1 rule*).

Cloning and evaluation of the library for bacterial surface display. Genomic DNA fragments were excised from the pMAL4.31 vector, containing the *S. pneumoniae* library with the restriction enzymes *Fse*I and *Not*I. The entire population of fragments was then transferred into plasmids pMAL9.1 (LamB) or pHIE11 (FhuA), which have been digested with *Fse*I and *Not*I. Using these two restriction enzymes, which recognise an 8 bp GC rich sequence, the reading frame that was selected in the pMAL4.31 vector is maintained in each of the platform vectors. The plasmid library was then transformed into *E. coli* DH5alpha cells by electroporation. Cells were plated onto large LB-agar plates supplemented with 50 µg/ml Kanamycin and grown over night at 37°C at a density yielding clearly visible single colonies. Cells were then scraped off the surface of these plates, washed with fresh LB medium and stored in aliquots for library screening at -80°C.

Results

Libraries for frame selection. Two libraries (LSPn70 and LSPn300) were generated in the pMAL4.31 vector with sizes of approximately 70 and 300 bp, respectively. For each library, ligation and subsequent transformation of approximately 1 µg of pMAL4.31 plasmid DNA and 50 ng of fragmented genomic *S. pneumoniae* DNA yielded 4x 10^5 to 2x 10^6 clones after frame selection. To assess the randomness of the libraries, approximately 600 randomly chosen clones of LSPn70 were sequenced. The bioinformatic analysis showed that of these clones only very few were present more than once. Furthermore, it was shown that 90% of the clones fell in the size range between 25 and 100 bp with an average size of 52 bp (Figure 2). Allmost all sequences followed the 3n+1 rule, showing that all clones were properly frame selected.

Bacterial surface display libraries. The display of peptides on the surface of *E. coli* required the transfer of the inserts from the LSPn libraries from the frame selection vector pMAL4.31 to the display plasmids pMAL9.1 (LamB) or pHIE11 (FhuA). Genomic DNA fragments were excised by *Fse*I and *Not*I restriction and ligation of 5ng inserts with 0.1µg plasmid DNA and subsequent transformation into DH5alpha cells resulted in 2-5x 10^6 clones. The clones were scraped off the LB plates and frozen without further amplification.

Example 3: Identification of highly immunogenic peptide sequences from *S. pneumoniae* using bacterial surface displayed genomic libraries and human serum

Experimental procedures

MACS screening. Approximately 2.5x 10^8 cells from a given library were grown in 5 ml LB-medium supplemented with 50 µg/ml Kanamycin for 2 h at 37°C. Expression was induced by the addition of 1 mM IPTG for 30 min. Cells were washed twice with fresh LB medium and approximately 2x 10^7 cells re-suspended in 100 µl LB medium and transferred to an Eppendorf tube.

10 µg of biotinylated, human IgGs purified from serum was added to the cells and the suspension incubated overnight at 4°C with gentle shaking. 900 µl of LB medium was added, the suspension mixed and subsequently centrifuged for 10 min at 6,000 rpm at 4°C (For IgA screens, 10 µg of purified IgAs were used and these captured with biotinylated anti-human-IgG secondary antibodies). Cells were washed once with 1 ml LB and then re-suspended in 100 µl LB medium. 10 µl of MACS microbeads coupled to streptavidin (Miltenyi Biotech, Germany) were added and the incubation continued for 20 min at 4°C. Thereafter 900 µl of LB medium was added and the MACS microbead cell suspension was loaded

onto the equilibrated MS column (Miltenyi Biotech, Germany) which was fixed to the magnet. (The MS columns were equilibrated by washing once with 1 ml 70% EtOH and twice with 2 ml LB medium.)

The column was then washed three times with 3 ml LB medium. After removal of the magnet, cells were eluted by washing with 2 ml LB medium. After washing the column with 3 ml LB medium, the 2 ml eluate was loaded a second time on the same column and the washing and elution process repeated. The loading, washing and elution process was performed a third time, resulting in a final eluate of 2 ml.

A second round of screening was performed as follows. The cells from the final eluate were collected by centrifugation and re-suspended in 1 ml LB medium supplemented with 50 μg/ml Kanamycin. The culture was incubated at 37°C for 90 min and then induced with 1 mM IPTG for 30 min. Cells were subsequently collected, washed once with 1 ml LB medium and suspended in 10 μl LB medium. 10 μg of human, biotinylated IgGs were added again and the suspension incubated over night at 4°C with gentle shaking. All further steps were exactly the same as in the first selection round. Cells selected after two rounds of selection were plated onto LB-agar plates supplemented with 50 μg/ml Kanamycin and grown over night at 37°C.

Evaluation of selected clones by sequencing and Western blot analysis. Selected clones were grown overnight at 37°C in 3 ml LB medium supplemented with 50 μg/ml Kanamycin to prepare plasmid DNA using standard procedures. Sequencing was performed at MWG (Germany) or in collaboration with TIGR (U.S.A.).

For Western blot analysis approximately 10 to 20 μg of total cellular protein was separated by 10% SDS-PAGE and blotted onto HybondC membrane (Amersham Pharmacia Biotech, England). The LamB or FhuA fusion proteins were detected using human serum as the primary antibody at a dilution of approximately 1:5,000 and anti-human IgG or IgA antibodies coupled to HRP at a dilution of 1:5,000 as secondary antibodies. Detection was performed using the ECL detection kit (Amersham Pharmacia Biotech, England). Alternatively, rabbit anti-FhuA or rabbit anti-LamB polyclonal immune sera were used as primary antibodies in combination with the respective secondary antibodies coupled to HRP for the detection of the fusion proteins.

Results

Screening of bacterial surface display libraries by magnetic activated cell sorting (MACS) using biotinylated Igs. The libraries LSPn70 in pMAL9.1 and LSPn300 in pHIE11 were screened with pools of biotinylated, human IgGs and IgAs from patient sera or sera from healthy individuals (see Example 1: *Preparation of antibodies from human serum*). The selection procedure was performed as described under Experimental procedures. Figure 3A shows a representative example of a screen with the LSPn-70 library and PSPn3-IgGs. As can be seen from the colony count after the first selection cycle from MACS screening, the total number of cells recovered at the end is drastically reduced from 2×10^7 cells to approximately 5×10^4 cells, whereas the selection without antibodies added showed a reduction to about 2×10^3 cells (Figure 3A). After the second round, a similar number of cells was recovered with PSPn3-IgGs, while fewer than 10 cells were recovered when no IgGs from human serum were added, clearly showing that selection was dependent on *S. pneumoniae* specific antibodies. To evaluate the performance of the screen, 26 selected clones were picked randomly and subjected to immunoblot analysis with screening IgG pool (PSPn7) (Figure 3B). This analysis revealed that ~90% of the selected clones showed reactivity with antibodies present in the relevant serum whereas the control strain expressing LamB without a *S. pneumoniae* specific insert did not react with the same serum. In general, the rate of reactivity was observed to lie within the range of 35 to 90%. Colony PCR analysis showed that all selected clones contained an insert in the expected size range.

Subsequent sequencing of a larger number of randomly picked clones (600 to 1200 per screen) led to the identification of the gene and the corresponding peptide or protein sequence that was specifically recognized by the human serum antibodies used for screening. The frequency with which a specific clone is selected reflects at least in part the abundance and/or affinity of the specific antibodies in the serum used for selection and recognizing the epitope presented by this clone. In that regard it is striking that clones derived from some ORFs (e.g. SP2216, SP0117, SP0641, SP2136, SP2190, SP0107, SP0082) were picked more than 100 times, indicating their highly immunogenic property. Table 1 summarizes the data obtained for all 12 performed screens. All clones that are presented in Table 1 have been verified by immunoblot analysis using whole cellular extracts from single clones to show the indicated reactivity with the pool of human serum used in the respective screen. As can be seen from Table 1, distinct regions of the identified ORF are identified as immunogenic, since variably sized fragments of the proteins are displayed on the surface by the platform proteins.

It is further worth noticing that most of the genes identified by the bacterial surface display screen encode proteins that are either attached to the surface of *S. pneumoniae* and/or are secreted. This is in accordance with the expected role of surface attached or secreted proteins in virulence of *S. pneumoniae.*

Example 4: Assessment of the reactivity of highly immunogenic peptide sequences with individual human sera.

Experimental procedures

Peptide synthesis

Peptides were synthesized in small scale (4 mg resin; up to 288 in parallel) using standard F-moc chemistry on a Rink amide resin (PepChem, Tübingen, Germany) using a SyroII synthesizer (Multisyntech, Witten, Germany). After the sequence was assembled, peptides were elongated with Fmoc-epsilon-aminohexanoic acid (as a linker) and biotin (Sigma, St. Louis, MO; activated like a normal amino acid). Peptides were cleaved off the resin with 93%TFA, 5% triethylsilane, and 2% water for one hour. Peptides were dried under vacuum and freeze dried three times from acetonitrile/water (1:1). The presence of the correct mass was verified by mass spectrometry on a Reflex III MALDI-TOF (Bruker, Bremen Germany). The peptides were used without further purification.

Enzyme linked immune assay (ELISA).

Biotin-labeled peptides (at the N-terminus) were coated on Streptavidin ELISA plates (EXICON) at 10 μg/ml concentration according to the manufacturer's instructions. Highly specific Horse Radish Peroxidase (HRP)-conjugated anti-human IgG secondary antibodies (Southern Biotech) were used according to the manufacturers' recommendations (dilution: 1,000x). Sera were tested at two serum dilutions, 200X and 1,000X. Following manual coating, peptide plates were processed and analyzed by the Gemini 160 ELISA robot (TECAN) with a built-in ELISA reader (GENIOS, TECAN).

Approximately 110 patients and 60 healthy adult sera were included in the analysis. Following the bioinformatic analysis of selected clones, corresponding peptides were designed and synthesized. In case of epitopes with more than 26 amino acid residues, overlapping peptides were made. All peptides were synthesized with a N-terminal biotin-tag and used as coating reagents on Streptavidin-coated ELISA plates.

The analysis was performed in two steps. First, peptides were selected based on their reactivity with the individual sera, which were included in the serum pools used for preparations of IgG and IgA screening reagents for bacterial surface display. A summary for serum reactivity of 224 peptides representing *S. pneumoniae* epitopes from the genomic screen analysed with 20 human sera (representing 4 different pools of five sera) used for the antigen identification is shown in Table 2. The peptides were compared by

the score calculated for each peptide based on the number of positive sera and the extent of reactivity. Peptides range from highly and widely reactive to weakly positive ones. Among the most reactive ones there are known antigens, some of them are also protective in animal challenge models for nasopharyngeal carriage or sepsis (e.g. PspA/SP0117, serine protease/SP0641, histidine triad protein/SP1175). Peptides not displaying a positive reaction were not included in further, more detailed studies.

Second, a large number of not pre-selected individual sera from patients with invasive pneumococcal disease or from healthy adults and children were tested against the peptides showing specific and high reactivity with the screening sera. Seroconversion during disease was tested for highly positive peptides by using three serial serum samples collected longitudinally from patients with invasive pneumococcal disease, the first before disease occurred (pre), the second in the acute phase (within 5 days after onset) and the third in the convalescent phase (> 3 weeks after onset) of the disease. Two representative ELISA experiments are shown with two different patients, displaying seroconversion to multiple peptides, suggesting that epitope-specific antibody levels were low before disease occurred, and were induced in the acute and convalescent phase (Fig. 5). The antigens showing this antibody profile are especially valuable for vaccine development (e.g. SP2216, SP2109, SP1175, SP0117, SP0082).

Example 5: Gene distribution studies with highly immunogenic proteins identified from *S. pneumoniae.*

Experimental procedures

Gene distribution of pneumococcal antigens by PCR. An ideal vaccine antigen would be an antigen that is present in all, or the vast majority of strains of the target organism to which the vaccine is directed. In order to establish whether the genes encoding the identified *Streptococcus pneumoniae* antigens occur ubiquitously in *S. pneumoniae* strains, PCR was performed on a series of independent *S. pneumoniae* isolates with primers specific for the gene of interest. *S. pneumoniae* isolates were obtained covering the serotypes most frequently present in patients as shown in Figure 4A. Oligonucleotide sequences as primers were designed for all identified ORFs yielding products of approximately 1,000 bp, if possible covering all identified immunogenic epitopes. Genomic DNA of all *S. pneumoniae* strains was prepared as described under Example 2. PCR was performed in a reaction volume of 25 μl using Taq polymerase (1U), 200 nM dNTPs, 10 pMol of each oligonucleotide and the kit according to the manufacturers instructions (Invitrogen, The Netherlands). As standard, 30 cycles (1x: 5min. 95°C, 30x: 30sec. 95°C, 30sec. 56°C, 30sec. 72°C, 1x 4min. 72°C) were performed, unless conditions had to be adapted for individual primer pairs.

Results

All identified genes encoding immunogenic proteins were tested by PCR for their presence in 50 different strains of *S. pneumoniae* (Figure 4A). As an example, figure 4B shows the PCR reaction for SP1604 with all indicated 50 strains. As clearly visible, the gene is present in all strains analysed. The PCR fragment from a type 14 strain was sequenced and showed that of 414 bp, 6 bp are different as compared to the *S. pneumoniae* type 4 strain, resulting in three amino acid difference between the two isolates.
From a total of 50 genes analysed, 31 were present in all strains tested, while 9 genes were absent in more than 10 of the tested 50 strains (Table 3). Several genes (SP0667, SP0930) showed variation in size and were not present in all strain isolates. Some genes showed variation in size, but were otherwise conserved in all tested strains. Sequencing of the generated PCR fragment from one strain and subsequent comparison to the type 4 strain confirmed the amplification of the correct DNA fragment and revealed a degree of sequence divergence as indicated in Table 3. Importantly, many of the identified antigens are well conserved in all strains in sequence and size and are therefore novel vaccine candidates to prevent

infections by pneumococci.

Example 6: Characterization of immune sera obtained from mice immunized with highly immunogenic proteins/peptides from *S. pneumoniae* displayed on the surface of *E. coli*.

Experimental procedures

Generation of immune sera from mice
E. coli clones harboring plasmids encoding the platform protein fused to a *S. pneumoniae* peptide, were grown in LB medium supplemented with 50µg/ml Kanamycin at 37°C. Overnight cultures were diluted 1:10, grown until an OD_{600} of 0.5 and induced with 0.2 mM IPTG for 2 hours. Pelleted bacterial cells were suspended in PBS buffer and disrupted by sonication on ice, generating a crude cell extract. According to the OD_{600} measurement, an aliquot corresponding to $5x10^7$ cells was injected into NMRI mice i.v., followed by a boost after 2 weeks. Serum was taken 1 week after the second injection. Epitope specific antibody levels were measured by peptide ELISA.

In vitro expression of antigens
Expression of antigens by *in vitro* grown *S. pneumoniae* serotype 4 was tested by immunoblotting. Different growth media and culture conditions were tested to detect the presence of antigens in total lysates and bacterial culture supernatants. Expression was considered confirmed when a specific band corresponding to the predicted molecular weight and electrophoretic mobility was detected.

Cell surface staining
Flow cytometric analysis was carried out as follows. Bacteria were grown under culture conditions, which resulted in expression of the antigen as shown by the immunoblot analysis. Cells were washed twice in Hanks Balanced Salt Solution (HBSS) and the cell density was adjusted to approximately 1 X 10^6 CFU in 100µl HBSS, 0.5% BSA. After incubation for 30 to 60 min at 4°C with mouse antisera diluted 50 to 100-fold, unbound antibodies were washed away by centrifugation in excess HBSS, 0.5% BSA. Secondary goat anti-mouse antibody ($F(ab')_2$ fragment specific) labeled with fluorescein (FITC) was incubated with the cells at 4°C for 30 to 60 min. After washing, cells were fixed with 2% paraformaldehyde. Bound antibodies were detected using a Becton Dickinson FACScan flow cytometer and data further analyzed with the computer program CELLQuest. Negative control sera included mouse pre-immune serum and mouse polyclonal serum generated with lysates prepared from IPTG induced *E. coli* cells transformed with plasmids encoding the genes *lamB* or *fhuA* without *S. pneumoniae* genomic insert.

Bactericidal (killing) assay
Murine macrophage cells (RAW246.7 or P388.D1) and bacteria were incubated and the loss of viable bacteria after 60 min was determined by colony counting. In brief, bacteria were washed twice in Hanks Balanced Salt Solution (HBSS) and the cell density was adjusted to approximately 1X 10^5 CFU in 50µl HBSS. Bacteria were incubated with mouse sera (up to 25%) and guinea pig complement (up to 5%) in a total volume of 100µl for 60min at 4°C. Pre-opsonized bacteria were mixed with macrophages (murine cell line RAW264.7 or P388.D1; 2X 10^6 cells per 100µl) at a 1:20 ratio and were incubated at 37°C on a rotating shaker at 500 rpm. An aliquot of each sample was diluted in sterile water and incubated for 5 min at room temperature to lyse macrophages. Serial dilutions were then plated onto Todd-Hewitt Broth agar plates. The plates were incubated overnight at 37°C, and the colonies were counted with the Countermat flash colony counter (IUL Instruments). Control sera included mouse pre-immune serum and mouse polyclonal serum generated with lysates prepared from IPTG induced *E. coli* transformed with plasmids harboring the genes *lamB* or *fhuA* without *S. pneumoniae* genomic insert.

Results

In vitro expression of antigens. The expression of the antigenic proteins was analyzed *in vitro* in *S.*

pneumoniae serotype 4 by using sera raised against *E. coli* clones harboring plasmids encoding the platform protein fused to a *S. pneumoniae* peptide. First, the presence of specific antibodies was determined by peptide ELISA and/or immunoblotting using the *E. coli* clone expressing the given epitope embedded in LamB or FhuA platform proteins. Positive sera were then analysed by immunblotting using total bacterial lysates and culture supernatants prepared from *S. pneumoniae* serotype 4 strain (data not shown). This analysis served as a first step to determine whether a protein is expressed at all, and if, under which growth conditions, in order to evaluate surface expression of the polypeptide by FACS analysis. It was anticipated based on literature data that not all proteins would be expressed under *in vitro* conditions.

Cell surface staining of S. pneumoniae. Cell surface accessibility for several antigenic proteins was subsequently demonstrated by an assay based on flow cytometry. Streptococci were incubated with preimmune and polyclonal mouse sera raised against *S. pneumoniae* lysate or *E. coli* clones harboring plasmids encoding the platform protein fused to a *S. pneumoniae* peptide, follow by detection with fluorescently tagged secondary antibody. As shown in Fig. 6A, antisera raised against *S. pneumoniae* lysate contains antibodies against surface components, demonstrated by a significant shift in fluorescence of the *S. pneumoniae* serotype 4 cell population. Similar cell surface staining of *S. pneumoniae* sertype 4 cells was observed with polyclonal sera raised against peptides of many of the pneumococcal antigens identified (Fig. 6B and Table 4.). In some instancies, a subpopulation of the bacteria was not stained, as indicated by the detection of two peaks in the histograms (Fig. 6B). This phenomenon may be a result of differential expression of the gene products during the growth of the bacterium, insufficient antibody levels or partial inhibition of antibody binding caused by other surface molecules or plasma proteins.

In vitro bactericidal activity. Opsonophagocytic killing is the cornerstone of host defense against extracellular bacteria, such as *S. pneumoniae.* Cell surface binding of antibodies to bacterial antigens are opsonizing and induce killing (bactericidal) by phagocytic cells (macrophages and neutrophil granulocytes) if the antibodies induced by the particular antigens can bind activated complement components (C3bi). It has been shown that anti-pneumococcal bactericidal activity of human sera measured in *in vitro* assays can be correlated with *in vivo* protection of vaccinated individuals {Romero-Steiner, S. et al., 1999}. In Figure 7 examples are shown and in Table 4 a summary is presented on bactericidal activity measured by antigen-specific antibodies generated in mice with corresponding epitopes. According to these data, several of the novel pneumococcal antigens induce functional antibodies (e.g. SP0082, SP2216, SP2136, SP0454, SP0069, SP0369, etc.). Importantly, a well-known protective pneumoniae antigen, PspA (SP0117) is proved to be strongly positive in the very same assay.

These experiments confirmed the bioinformatic prediction that many of the proteins are exported due to their signal peptide sequence and in addition showed that they are present on the cell surface of *S. pneumoniae* serotype 4. They also confirm that these proteins are available for recognition by human antibodies with functional properties and make them valuable candidates for the development of a vaccine against pneumococcal diseases.

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Table 1: Immunogenic proteins identified by bacterial surface display.

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq: ID (DNA, Prot.)
SP0008	hypothetical protein	4-11,35-64,66-76,101-108,111-119	G:15	57-114	1, 145
SP0032	DNA polymerase I (polA)	5-27,32-64,92-102,107-113,119-125,133-139,148-162,177-187,195-201,207-214,241-251,254-269,285-300,302-309,317-324,332-357,365-404,411-425,443-463,470-477,479-487,506-512,515-520,532-547,556-596,603-610,616-622,624-629,636-642,646-665,667-674,687-692,708-720,734-739,752-757,798-820,824-851,856-865	H:39, I:6, L:2	732-763	2, 146
SP0069	Choline binding protein I	14-21,36-44,49-66,102-127,162-167,177-196	G:1, H:2, I:1, K:44, L:3, M:1	45-109 145-172	3, 147
SP0071	immunoglobulin A1 protease (iga-1)	17-35,64-75,81-92,100-119,125-172,174-183,214-222,230-236,273-282,287-303,310-315,331-340,392-398,412-420,480-505,515-523,525-546,553-575,592-598,603-609,617-625,631-639,644-651,658-670,681-687,691-704,709-716,731-736,739-744,750-763,774-780,784-791,799-805,809-822,859-870,880-885,907-916,924-941,943-949,973-986,1010-1016,1026-1036,1045-1054,1057-1062,1082-1088,1095-1102,1109-1120,1127-1134,1140-1146,1152-1159,1169-1179,1187-1196,1243-1251,1262-1273,1279-1292,1306-1312,1332-1343,1348-1364,1379-1390,1412-1420,1427-1436,1458-1468,1483-1503,1524-1549,1574-1588,1614-1619,1672-1685,1697-1707,1711-1720,1738-1753,1781-1787,1796-1801,1826-1843	A:3, C:1, D:9, E:9, F:4, G:21, I:34, K:61, L:20, M:2	132-478 508-592 1753-1810	4, 148
SP0082	Cell wall surface anchor	15-43,49-55,71-77,104-110,123-130,162-171,180-192,199-205,219-227,246-254,264-270,279-287,293-308,312-322,330-342,349-356,369-377,384-394,401-406,416-422,432-439,450-460,464-474,482-494,501-508,521-529,536-546,553-558,568-574,584-591,602-612,616-626,634-646,653-660,673-681,688-698,705-710,720-726,736-749,833-848	C:9, E:4, F:2, I:26, L:4, M:67	1-199 200-337 418-494 549-647	5, 149
SP0107	LysM domain protein	9-30,65-96,99-123,170-178	A :3, B :16, C :15, D :1, E :5, F :178, M :1	1-128	6, 150

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
SP0117	pneumococcal surface protein A (pspA)	7-32,34-41,96-106,127-136,154-163,188-199,207-238,272-279,306-312,318-325,341-347,353-360,387-393,399-406,434-440,452-503,575-580,589-601,615-620,635-640,654-660,674-680,696-701,710-731	A:13, B:11, C:10, D:4, E:31, F:6, G:33, H:13, I:9, K:64, L:32, M:46	1-548 660-691	7, 151
SP0191	hypothetical protein	4-19,35-44,48-59,77-87,93-99,106-111,130-138,146-161	E:1, I:2	78-84	8, 152
SP0197	dihydrofolate synthetase, putative	24-30,36-43,64-86,93-99,106-130,132-145,148-165,171-177,189-220,230-249,251-263,293-300,302-312,323-329,338-356,369-379,390-412	L :9	179-193	9, 153
SP0212	Ribosomal protein L2	30-39,61-67,74-81,90-120,123-145,154-167,169-179,182-197,200-206,238-244,267-272	L:10	230-265	10, 154
SP0222	Ribosomal protein S14	14-20,49-65,77-86	H:14, L:8, M:3	2-68	11, 155
SP0239	Conserved hypothetical protein	4-9,26-35,42-48,53-61,63-85,90-101,105-111,113-121,129-137,140-150,179-188,199-226,228-237,248-255,259-285,299-308,314-331,337-343,353-364,410-421,436-442	L:2, M:1	110-144	12, 156
SP0251	formate acetyltransferase, putative	36-47,55-63,94-108,129-134,144-158,173-187,196-206,209-238,251-266,270-285,290-295,300-306,333-344,346-354,366-397,404-410,422-435,439-453,466-473,515-523,529-543,554-569,571-585,590-596,607-618,627-643,690-696,704-714,720-728,741-749,752-767,780-799	G:2, H:7, I:1, M:5	225-247 480-507	13, 157
SP0295	ribosomal protein S9 (rpsI)	16-25,36-70,80-93,100-106	I:4	78-130	14, 158
SP0330	sugar binding transcriptional regulator RegR	18-27,41-46,50-57,65-71,79-85,93-98,113-128,144-155,166-178,181-188,201-207,242-262,265-273,281-295,303-309,318-327	G:1, H:1, L:4	36-64	15, 159
SP0368	cell wall surface anchor family protein	7-29,31-44,50-59,91-96,146-153,194-201,207-212,232-238,264-278,284-290,296-302,326-353,360-370,378-384,400-405,409-418,420-435,442-460,499-506,529-534,556-562,564-576,644-651,677-684,687-698,736-743,759-766,778-784,808-814,852-858,874-896,920-925,929-935,957-965,1003-1012,1021-1027,1030-1044,1081-1087,1101-1111,1116-1124,1148-1159,1188-1196,1235-1251,1288-1303,1313-1319,1328-1335,1367-1373,1431-1437,1451-1458,1479-1503,1514-1521,1530-	D:1, H:3, I:1, L:1, M:3	1-70 154-189 922-941 1445-1462 1483-1496	16, 160

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		1540,1545-1552,1561-1568,1598-1605,1617-1647,1658-1665,1670-1676,1679-1689,1698-1704,1707-1713,1732-1738,1744-1764			
SP0369	Penicillin binding protein 1A	6-51,81-91,104-113,126-137,150-159,164-174,197-209,215-224,229-235,256-269,276-282,307-313,317-348,351-357,376-397,418-437,454-464,485-490,498-509,547-555,574-586,602-619	B:1, E:1, L:13, M:1	452-530	17, 161
SP0374	hypothetical protein	25-31,39-47,49-56,99-114,121-127,159-186,228-240,253-269,271-279,303-315,365-382,395-405,414-425,438-453	E:4, I:1, L:3	289-384	18, 162
SP0377	Choline binding protein C	9-24,41-47,49-54,68-78,108-114,117-122,132-140,164-169,179-186,193-199,206-213,244-251,267-274,289-294,309-314,327-333	G:5, H:4, I:1, K:88, L:3, M:8	209-249 286-336	19, 163
SP0378	choline binding protein J (cbpJ)	9-28,53-67,69-82,87-93,109-117,172-177,201-207,220-227,242-247,262-268,305-318,320-325	K:47, L:6, M:5	286-306	20, 164
SP0390	choline binding protein G (cbpG)	4-10,26-39,47-58,63-73,86-96,98-108,115-123,137-143,148-155,160-176,184-189,194-204,235-240,254-259,272-278	G:1, K:69, M:6	199-283	21, 165
SP0454	hypothetical protein	4-26,33-39,47-53,59-65,76-83,91-97,104-112,118-137,155-160,167-174,198-207,242-268,273-279,292-315,320-332,345-354,358-367,377-394,403-410,424-439,445-451,453-497,511-518,535-570,573-589,592-601,604-610	H:1, I:1, L:6	202-242	22, 166
SP0463	cell wall surface anchor family protein	8-30,36-45,64-71,76-82,97-103,105-112,134-151,161-183,211-234,253-268,270-276,278-284,297-305,309-315,357-362,366-372,375-384,401-407,409-416,441-455,463-470,475-480,490-497,501-513,524-537,552-559,565-576,581-590,592-600,619-625,636-644,646-656	A:1, B:2, C:4, E:1, F:4,	316-419	23, 167
SP0466	sortase, putative	4-17,52-58,84-99,102-110,114-120,124-135,143-158,160-173,177-196,201-216,223-250,259-267,269-275	E:1, M:2	1-67	24, 168
SP0468	Sortase, putative	6-46,57-67,69-80,82-133,137-143,147-168,182-187,203-209,214-229,233-242,246-280	G:24, H:20, L:1	53-93	25, 169
SP0498	endo-beta-N-acetylglucosaminidase, putative	7-40,50-56,81-89,117-123,202-209,213-218,223-229,248-261,264-276,281-288,303-308,313-324,326-332,340-346,353-372,434-443,465-474,514-523,556-564,605-616,620-626,631-636,667-683,685-699,710-719,726-732,751-756,760-771,779-788,815-828,855-867,869-879,897-902,917-924,926-931,936-942,981-1000,1006-1015,1017-1028,1030-1039,1046-1054,1060-1066,1083-1092,1099-1112,1122-1130,1132-1140,1148-1158,1161-	B:5, C:1, E:2, F:1, G:2	1226-1309 1455-1536 1538-1605	26, 170

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		1171,1174-1181,1209-1230,1236-1244,1248-1254,1256-1267,1269-1276,1294-1299,1316-1328,1332-1354,1359-1372,1374-1380,1384-1390,1395-1408,1419-1425,1434-1446,1453-1460,1465-1471,1474-1493,1505-1515,1523-1537,1547-1555,1560-1567,1577-1605,1633-1651			
SP0509	type I restriction-modification system, M subunit	4-10,31-39,81-88,106-112,122-135,152-158,177-184,191-197,221-227,230-246,249-255,303-311,317-326,337-344,346-362,365-371,430-437,439-446,453-462,474-484	I:2	449-467	27, 171
SP0519	dnaJ protein (dnaJ)	9-15,24-35,47-55,122-128,160-177,188-196,202-208,216-228,250-261,272-303,318-324,327-339,346-352,355-361,368-373	A:1, D:2, H:2	108-218 344-376	28, 172
SP0529	BlpC ABC transporter (blpB)	6-14,17-48,55-63,71-90,99-109,116-124,181-189,212-223,232-268,270-294,297-304,319-325,340-348,351-370,372-378,388-394,406-415,421-434	A:1, B:3, C:3, D:1, F:4,	177-277	29, 173
SP0564	hypothetical protein	21-39,42-61,65-75,79-85,108-115	H:3	11-38	30, 174
SP0609	amino acid ABC transporter, amino acid-binding protein	4-17,26-39,61-76,103-113,115-122,136-142,158-192,197-203,208-214,225-230,237-251	I:3	207-225	31, 175
SP0613	metallo-beta-lactamase superfamily protein	5-11,27-36,42-53,62-70,74-93,95-104,114-119,127-150,153-159,173-179,184-193,199-206,222-241,248-253,257-280,289-295,313-319,322-342,349-365,368-389,393-406,408-413,426-438,447-461,463-470,476-495,532-537,543-550	I:12	225-246	32, 176
SP0641	Serine protease	4-29,68-82,123-130,141-147,149-157,178-191,203-215,269-277,300-307,327-335,359-370,374-380,382-388,393-400,410-417,434-442,483-492,497-503,505-513,533-540,564-569,601-607,639-647,655-666,693-706,712-718,726-736,752-758,763-771,774-780,786-799,806-812,820-828,852-863,884-892,901-909,925-932,943-948,990-996,1030-1036,1051-1059,1062-1068,1079-1086,1105-1113,1152-1162,1168-1179,1183-1191,1204-1210,1234-1244,1286-1295,1318-1326,1396-1401,1451-1460,1465-1474,1477-1483,1488-1494,1505-1510,1514-1521,1552-1565,1593-1614,1664-1672,1677-1685,1701-1711,1734-1745,1758-1770,1784-1798,1840-1847,1852-1873,1885-1891,1906-1911,1931-1939,1957-1970,1977-1992,2014-2020,2026-2032,2116-2134	A:19, B:72, C:34, D:5, E:21, F:86, G:26, H:86, I:17, L:130, M:29	1-348 373-490 573-767 903-1043 1155-1198 1243-1482 1550-1595 1682-1719 1793-1921 2008-2110	33, 177
SP0648	beta-galactosidase (bgaA)	10-35,39-52,107-112,181-188,226-236,238-253,258-268,275-284,296-310,326-338,345-368,380-389,391-	C:1, E:1, F:1, G:1,	1526-1560	34, 178

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		408,410-418,420-429,444-456,489-505,573-588,616-623,637-643,726-739,741-767,785-791,793-803,830-847,867-881,886-922,949-956,961-980,988-1004,1009-1018,1027-1042,1051-1069,1076-1089,1108-1115,1123-1135,1140-1151,1164-1179,1182-1191,1210-1221,1223-1234,1242-1250,1255-1267,1281-1292,1301-1307,1315-1340,1348-1355,1366-1373,1381-1413,1417-1428,1437-1444,1453-1463,1478-1484,1490-1496,1498-1503,1520-1536,1538-1546,1548-1570,1593-1603,1612-1625,1635-1649,1654-1660,1670-1687,1693-1700,1705-1711,1718-1726,1729-1763,1790-1813,1871-1881,1893-1900,1907-1935,1962-1970,1992-2000,2006-2013,2033-2039,2045-2051,2055-2067,2070-2095,2097-2110,2115-2121,2150-2171,2174-2180,2197-2202,2206-2228	H:4, I:1, M:2		
SP0664	Zinc metalloprotease ZmpB, putative	4-17,35-48,54-76,78-107,109-115,118-127,134-140,145-156,169-174,217-226,232-240,256-262,267-273,316-328,340-346,353-360,402-409,416-439,448-456,506-531,540-546,570-578,586-593,595-600,623-632,662-667,674-681,689-705,713-724,730-740,757-763,773-778,783-796,829-835,861-871,888-899,907-939,941-955,957-969,986-1000,1022-1028,1036-1044,1068-1084,1095-1102,1118-1124,1140-1146,1148-1154,1168-1181,1185-1190,1197-1207,1218-1226,1250-1270,1272-1281,1284-1296,1312-1319,1351-1358,1383-1409,1422-1428,1438-1447,1449-1461,1482-1489,1504-1510,1518-1527,1529-1537,1544-1551,1569-1575,1622-1628,1631-1637,1682-1689,1711-1718,1733-1740,1772-1783,1818-1834,1859-1872	A:9, B:25, C:13, D:7, E:14, F:77, G:12, H:10, K:67, L:13, M:6	1-64 128-495	35, 179
SP0667	pneumococcal surface protein, putative	8-28,32-37,62-69,119-125,137-149,159-164,173-189,200-205,221-229,240-245,258-265,268-276,287-293,296-302,323-329	A:72, B:80, C:90, D:20, E:12, F:53	1-95	36, 180
SP0688	UDP-N-acetylmuramoylalanine--D-glutamate ligase	9-18,25-38,49-63,65-72,74-81,94-117,131-137,139-146,149-158,162-188,191-207,217-225,237-252,255-269,281-293,301-326,332-342,347-354,363-370,373-380,391-400,415-424,441-447	I:3	75-107	37, 181
SP0749	branched-chain amino acid ABC transporter	4-24,64-71,81-87,96-116,121-128,130-139,148-155,166-173,176-184,203-215,231-238,243-248,256-261,280-286,288-306,314-329	E:2, I:8, L:8	67-148	38, 182
SP0770	ABC transporter,	4-10,19-37,46-52,62-81,83-89,115-120,134-139,141-	L:2	404-420	39, 183

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
	ATP-binding protein	151,168-186,197-205,209-234,241-252,322-335,339-345,363-379,385-393,403-431,434-442,447-454,459-465,479-484,487-496			
SP0785	conserved hypothetical protein	10-35,46-66,71-77,84-93,96-122,138-148,154-172,182-213,221-233,245-263,269-275,295-301,303-309,311-320,324-336,340-348,351-359,375-381	C:1, E:2, I:1	111-198	40, 184
SP0914	nodulin-related protein, truncation	14-25,30-42,47-61,67-75,81-91,98-106,114-122,124-135,148-193,209-227	L.2	198-213	41, 185
SP0930	choline binding protein E (cbpE)	5-18,45-50,82-90,97-114,116-136,153-161,163-171,212-219,221-227,240-249,267-281,311-317,328-337,375-381,390-395,430-436,449-455,484-495,538-543,548-554,556-564,580-586,596-602	E:4, G:2, H:1, I:2, K:5	493-606	42, 186
SP0943	Gid protein (gid)	9-25,28-34,37-44,61-68,75-81,88-96,98-111,119-133,138-150,152-163,168-182,186-194,200-205,216-223,236-245,257-264,279-287,293-304,311-318,325-330,340-346,353-358,365-379,399-409,444-453	E:2, L:24	303-391	43, 187
SP0952	alanine dehydrogenase, authentic frameshift (ald)	16-36,55-61,66-76,78-102,121-130,134-146,150-212,221-239,255-276,289-322,329-357	G:3, H:4	29-59	44, 188
SP1003	conserved hypothetical protein (PAT)	8-27,68-74,77-99,110-116,124-141,171-177,202-217,221-228,259-265,275-290,293-303,309-325,335-343,345-351,365-379,384-394,406-414,423-437,452-465,478-507,525-534,554-560,611-624,628-651,669-682,742-747,767-778,782-792,804-812,820-836	A:2, B:5, C:8, D:5, E:13, F:3, M:2	79-231 359-451	45, 189
SP1004	Conserved hypothetical protein	5-28,39-45,56-62,67-74,77-99,110-117,124-141,168-176,200-230,237-244,268-279,287-299,304-326,329-335,348-362,370-376,379-384,390-406,420-429,466-471,479-489,495-504,529-541,545-553,561-577,598-604,622-630,637-658,672-680,682-688,690-696,698-709,712-719,724-736,738-746,759-769,780-786,796-804,813-818,860-877,895-904,981-997,1000-1014,1021-1029	A:5, B:4, C:4, D:9, E:12, F:4, H:3, I:1, L:1	1-162 206-224 254-350 414-514 864-938	46, 190
SP1124	glycogen synthase (glgA)	4-11,19-49,56-66,68-101,109-116,123-145,156-165,177-185,204-221,226-234,242-248,251-256,259-265,282-302,307-330,340-349,355-374,377-383,392-400,422-428,434-442,462-474	M:1	266-322	47, 191
SP1154	IgA1 protease	14-43,45-57,64-74,80-87,106-127,131-142,145-161,173-180,182-188,203-210,213-219,221-243,245-254,304-	A:6, B:2, C:9, D:3,	172-354 384-448	48, 192

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		311,314-320,342-348,354-365,372-378,394-399,407-431,436-448,459-465,470-477,484-490,504-509,531-537,590-596,611-617,642-647,723-734,740-751,754-762,764-774,782-797,807-812,824-831,838-845,877-885,892-898,900-906,924-935,940-946,982-996,1006-1016,1033-1043,1051-1056,1058-1066,1094-1108,1119-1126,1129-1140,1150-1157,1167-1174,1176-1185,1188-1201,1209-1216,1220-1228,1231-1237,1243-1248,1253-1285,1288-1297,1299-1307,1316-1334,1336-1343,1350-1359,1365-1381,1390-1396,1412-1420,1427-1439,1452-1459,1477-1484,1493-1512,1554-1559,1570-1578,1603-1608,1623-1630,1654-1659,1672-1680,1689-1696,1705-1711,1721-1738,1752-1757,1773-1780,1817-1829,1844-1851,1856-1863,1883-1895,1950-1958,1974-1990	E:4, F:2, G:6, H:4, I:13, L:12	464-644 648-728 1357-1370	
SP1174	conserved domain protein (PAT)	8-27,68-74,77-99,110-116,124-141,169-176,201-216,220-227,258-264,274-289,292-302,308-324,334-342,344-350,364-372,377-387,399-407,416-429,445-458,471-481,483-500,518-527,547-553,604-617,621-644,662-675,767-778,809-816	B:14, C:17, D:6, E:18, F:16, I:1, K:5, L:1, M:8	15-307 350-448 496-620	49, 193
SP1175	conserved domain protein	4-17,24-29,53-59,62-84,109-126,159-164,189-204,208-219,244-249,274-290,292-302,308-324,334-342,344-350,378-389,391-397,401-409,424-432,447-460,470-479,490-504,521-529,538-544,549-555,570-577,583-592,602-608,615-630,635-647,664-677,692-698,722-731,733-751,782-790,793-799	A:1, B:4, C:3, D:3, E:9, F:2, H:2, M:4	56-267 337-426 495-601	50, 194
SP1221	type II restriction endonuclease	12-22,49-59,77-89,111-121,136-148,177-186,207-213,217-225,227-253,259-274,296-302,328-333,343-354,374-383,424-446,448-457,468-480,488-502,507-522,544-550,553-560,564-572,587-596,604-614,619-625,629-635,638-656,662-676,680-692,697-713,720-738,779-786,833-847,861-869,880-895,897-902,911-917,946-951,959-967,984-990,992-1004,1021-1040,1057-1067,1073-1080	G:2, H:1, K:1, L:4	381-403	51, 195
SP1227	DNA-binding response regulator	4-10,26-31,46-56,60-66,70-79,86-94,96-102,109-118,132-152,164-187,193-206,217-224	E:1, L:3	81-149	52, 196
SP1241	amino acid ABC transporter, amino acid-binding pro	4-21,26-37,48-60,71-82,109-117,120-128,130-136,142-147,181-187,203-211,216-223,247-255,257-284,316-325,373-379,395-400,423-435,448-456,479-489,512-576,596-625,641-678,680-688,692-715	B:2, C:1, E:2, I:1	346-453	53, 197

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
SP1287	signal recognition particle protein (ffh)	10-16,25-31,34-56,58-69,71-89,94-110,133-176,186-193,208-225,240-250,259-266,302-307,335-341,376-383,410-416	B :8, G :8, H :3, M :1	316-407	54, 198
SP1330	N-acetylmannosamine-6-P epimerase, putative (nanE)	11-29,42-56,60-75,82-88,95-110,116-126,132-143,145-160,166-172,184-216	L:45	123-164	55, 199
SP1374	Chorismate sythetase (aroC)	11-29,54-63,110-117,139-152,158-166,172-180,186-193,215-236,240-251,302-323,330-335,340-347,350-366,374-381	G:1, L:29, M:14	252-299	56, 200
SP1378	conserved hypothetical protein	18-27,35-42,50-56,67-74,112-136,141-153,163-171,176-189,205-213,225-234,241-247,253-258,269-281,288-298,306-324,326-334,355-369,380-387	H:2	289-320	57, 201
SP1429	peptidase, U32 family	7-15,19-41,56-72,91-112,114-122,139-147,163-183,196-209,258-280,326-338,357-363,391-403,406-416	H:4	360-378	58, 202
SP1478	oxidoreductase, aldo/keto reductase family	11-18,29-41,43-49,95-108,142-194,204-212,216-242,247-256,264-273	H:11	136-149	59, 203
SP1518	conserved hypothetical protein	18-24,33-40,65-79,89-102,113-119,130-137,155-161,173-179,183-203,205-219,223-231;245-261,267-274;296-306,311-321,330-341,344-363,369-381,401-408,415-427,437-444,453-464,472-478,484-508,517-524,526-532,543-548	A:10, E:4, G:5, H:1	59-180	60, 204
SP1522	conserved domain protein	5-13,52-65,67-73,97-110,112-119,134-155	B:4, C:6, E:1, H:7, L:3	45-177	61, 205
SP1527	oligopeptide ABC transporter	6-28,34-43,57-67,75-81,111-128,132-147,155-163,165-176,184-194,208-216,218-229,239-252,271-278,328-334,363-376,381-388,426-473,481-488,492-498,507-513,536-546,564-582,590-601,607-623	A:1, B:1, C:4, F:1, G:26, H:18, I:10, L:2, M:1	148-269 420-450 610-648	62, 206
SP1573	lysozyme (lytC)	4-12,20-38,69-75,83-88,123-128,145-152,154-161,183-188,200-213,245-250,266-272,306-312,332-339,357-369,383-389,395-402,437-453,455-470,497-503	A:40, B:27, C:24, D:2, E:6, G:11, K:1	1-112	63, 207
SP1604	hypothetical protein	35-59,74-86,111-117,122-137	A:1, C:3, E:1, G:1, I:1	70-154	64, 208
SP1661	cell division protein	26-42,54-61,65-75,101-107,123-130,137-144,148-	E :2	157-249	65, 209

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
	DivIVA	156,164-172,177-192,213-221,231-258			
SP1664	ylmF protein (ylmF)	29-38,61-67,77-87,94-100,105-111,118-158	B:1, C:42, I:3	1-97	66, 210
SP1676	N-acetylneuraminate lyase, putative	7-21,30-48,51-58,60-85,94-123,134-156,160-167,169-183,186-191,216-229,237-251,257-267,272-282,287-298	H:2	220-243	67, 211
SP1687	neuraminidase B (nanB)	6-29,34-47,56-65,69-76,83-90,123-134,143-151,158-178,197-203,217-235,243-263,303-309,320-333,338-348,367-373,387-393,407-414,416-427,441-457,473-482,487-499,501-509,514-520,530-535,577-583,590-602,605-612,622-629,641-670,678-690	B:3, E:2, L:1, M:2	37-71 238-307	68, 212
SP1693	neuraminidase A (nanA)	7-40,121-132,148-161,196-202,209-215,221-235,248-255,271-280,288-295,330-339,395-409,414-420,446-451,475-487,556-563,568-575,580-586,588-595,633-638,643-648,652-659,672-685,695-700,710-716,737-742,749-754,761-767,775-781,796-806,823-835,850-863,884-890,892-900,902-915,934-941	C:3, D:5, E:3, F:1, G:7, H:1, I:3, K:20, L:4	406-521	69, 213
SP1732	serine/threonine protein kinase	9-18,24-46,51-58,67-77,85-108,114-126,129-137,139-146,152-165,173-182,188-195,197-204,217-250,260-274,296-313,343-366,368-384,427-434,437-446,449-455,478-484,492-506,522-527,562-591,599-606,609-618,625-631,645-652	E:2, H:1	577-654	70, 214
SP1735	methionyl-tRNA formyltransferase (fmt)	13-20,26-37,41-53,56-65,81-100,102-114,118-127,163-188,196-202,231-238,245-252,266-285,293-298,301-306	K:13, M:13	19-78	71, 215
SP1759	preprotein translocase, SecA subunit (secA-2)	10-23,32-42,54-66,73-91,106-113,118-127,139-152,164-173,198-207,210-245,284-300,313-318,330-337,339-346,354-361,387-393,404-426,429-439,441-453,467-473,479-485,496-509,536-544,551-558,560-566,569-574,578-588,610-615,627-635,649-675,679-690,698-716,722-734,743-754,769-780,782-787	I:6, L:2, M:2	480-550	72, 216
SP1772	cell wall surface anchor family protein	6-39,42-50,60-68,76-83,114-129,147-162,170-189,197-205,217-231,239-248,299-305,338-344,352-357,371-377,380-451,459-483,491-499,507-523,537-559,587-613,625-681,689-729,737-781,785-809,817-865,873-881,889-939,951-975,983-1027,1031-1055,1063-1071,1079-1099,1103-1127,1151-1185,1197-1261,1269-1309,1317-1333,1341-1349,1357-1465,1469-1513,1517-1553,1557-1629,1637-1669,1677-1701,1709-1725,1733-1795,1823-1849,1861-1925,1933-1973,1981-2025,2029-	B:9, C:1, D:1, F:13, G:1, H:3, I:1, L:1, M:2	74-171 452-559 2951-3061	73, 217

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		2053,2061-2109,2117-2125,2133-2183,2195-2219,2227-2271,2275-2299,2307-2315,2323-2343,2347-2371,2395-2429,2441-2529,2537-2569,2577-2601,2609-2625,2633-2695,2699-2737,2765-2791,2803-2867,2889-2913,2921-2937,2945-2969,2977-2985,2993-3009,3023-3045,3073-3099,3111-3167,3175-3215,3223-3267,3271-3295,3303-3351,3359-3367,3375-3425,3437-3461,3469-3513,3517-3541,3549-3557,3565-3585,3589-3613,3637-3671,3683-3747,3755-3795,3803-3819,3827-3835,3843-3951,3955-3999,4003-4039,4043-4115,4123-4143,4147-4171,4195-4229,4241-4305,4313-4353,4361-4377,4385-4393,4401-4509,4513-4557,4561-4597,4601-4718,4749-4768			
SP1804	general stress protein 24, putative	16-22,30-51,70-111,117-130,137-150,171-178,180-188,191-196	I:4	148-181	74, 218
SP1888	oligopeptide ABC transporter, ATP-binding protein AmiE	6-19,21-46,50-56,80-86,118-126,167-186,189-205,211-242,244-267,273-286,290-297,307-316,320-341	H:1	34-60	75, 219
SP1891	oligopeptide ABC transporter,	5-26,33-43,48-54,58-63,78-83,113-120,122-128,143-152,157-175,185-192,211-225,227-234,244-256,270-281,284-290,304-310,330-337,348-355,362-379,384-394,429-445,450-474,483-490,511-520,537-546,548-554,561-586,590-604,613-629	A:2, B:3, E:1, F:1, G:13, H:8	149-186 285-431 573-659	76, 220
SP1937	Autolysin (lytA)	5-26,49-59,61-67,83-91,102-111,145-157,185-192,267-272,279-286,292-298,306-312	D:3, F:1, G:1, H:2, K:11, M:1	134-220 235-251 254-280	77, 221
SP1954	serine protease, subtilase family, authentic frame	5-19,72-79,83-92,119-124,140-145,160-165,167-182,224-232,240-252,259-270,301-310,313-322,332-343,347-367,384-398,416-429,431-446,454-461	C:43, E:6, I:4, K:21, L:50	1-169	78, 222
SP1980	cmp-binding-factor 1 (cbf1)	8-17,26-31,56-62,75-83,93-103,125-131,135-141,150-194,205-217,233-258,262-268,281-286	H:9	127-168	79, 223
SP1992	cell wall surface anchor family protein	6-12,69-75,108-115,139-159,176-182,194-214	B:5, C:1, F:4, I:1	46-161	80, 224
SP1999	catabolite control protein A (ccpA)	6-13,18-27,39-48,51-59,66-73,79-85,95-101,109-116,118-124,144-164,166-177,183-193,197-204,215-223,227-236,242-249,252-259,261-270,289-301,318-325	I:2	12-58	81, 225
SP2021	glycosyl hydrolase	4-10,26-32,48-60,97-105,117-132,138-163,169-185,192-214,219-231,249-261,264-270,292-308,343-356,385-392,398-404,408-417,435-441	L:3	24-50	82, 226
SP2027	Conserved	10-40,42-48,51-61,119-126	A:1, E:1,	1-118	83, 227

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
	hypothetical protein		G:19, H:12, I:16, L:5		
SP2039	conserved hypothetical protein	5-17,40-58,71-83,103-111,123-140,167-177,188-204	G:1, L:3	116-128	84, 228
SP2048	Conserved hypothetical protein	4-9,11-50,57-70,112-123,127-138	I:1, L:4	64-107	85, 229
SP2051	Conpetence protein CglC	9-39,51-67	D:1, G:3, I:8, L:26	1-101	86, 230
SP2092	UTP-glucose-1-phosphate uridylyltransferase (galU)	5-14,17-25,28-46,52-59,85-93,99-104,111-120,122-131,140-148,158-179,187-197,204-225,271-283,285-293	H:2	139-155	87, 231
SP2099	Penicillin binding protein 1B	42-70,73-90,92-108,112-127,152-164,166-172,181-199,201-210,219-228,247-274,295-302,322-334,336-346,353-358,396-414,419-425,432-438,462-471,518-523,531-536,561-567,576-589,594-612,620-631,665-671,697-710,718-731,736-756,765-771,784-801	A:1, B:9, C:11, D:1, E:6, F:1, H:4, K:1	626-653	88, 232
SP2108	Maltose ABC transporter	8-28,41-51,53-62,68-74,79-85,94-100,102-108,114-120,130-154,156-162,175-180,198-204,206-213,281-294,308-318,321-339,362-368,381-386,393-399,407-415	G:10, H:1, L:10, M:1	2-13	89, 233
SP2120	hypothetical protein	4-39,48-65,93-98,106-112,116-129	I:2	10-36	90, 234
SP2128	transketolase, N-terminal subunit	25-32,35-50,66-71,75-86,90-96,123-136,141-151,160-179,190-196,209-215,222-228,235-242,257-263,270-280	H:2	209-247	91, 235
SP2136	choline binding protein PcpA	5-29,31-38,50-57,62-75,83-110,115-132,168-195,197-206,216-242,249-258,262-269,333-340,342-350,363-368,376-392,400-406,410-421,423-430,436-442,448-454,460-466,471-476,491-496,511-516,531-536,551-556,571-576,585-591,599-605	C:3, F:1, G:24, H:32, I:13, K:177, L:34, M:18	27-70 219-293 441-504 512-584	92, 236
SP2141	glycosyl hydrolase-related protein	4-12,14-34,47-75,83-104,107-115,133-140,148-185,187-196,207-212,224-256,258-265,281-287,289-296,298-308,325-333,345-355,365-371,382-395,424-435,441-457,465-472,483-491,493-505,528-534,536-546,552-558,575-584,589-600,616-623	L:3	576-591	93, 237
SP2180	conserved hypothetical protein	4-76, 78-89, 91-126, 142-148, 151-191, 195-208, 211-223, 226-240, 256-277, 279-285, 290-314, 317-323, 358-377, 381-387, 391-396, 398-411, 415-434, 436-446, 454-484, 494-512, 516-523, 538-552, 559-566, 571-577, 579-596, 599-615, 620-627, 635-644, 694-707, 720-734, 737-759, 761-771	I:3	313-329	94, 238

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
SP2190	choline binding protein A (cbpA)	7-38,44-49,79-89,99-108,117-123,125-132,137-146,178-187,207-237,245-255,322-337,365-387,398-408,445-462,603-608,623-628,644-650,657-671,673-679	A:6, B:12, C:9, D:6, E:30, F:8, G:65, H:72, I:76, K:222, L:99, M:37	111-566	95, 239
SP2194	ATP-dependent Clp protease, ATP-binding subunit	6-20,22-35,39-45,58-64,77-117,137-144,158-163,205-210,218-224,229-236,239-251,263-277,299-307,323-334,353-384,388-396,399-438,443-448,458-463,467-478,481-495,503-509,511-526,559-576,595-600,612-645,711-721,723-738,744-758,778-807	H:1	686-720	96, 240
SP2201	choline binding protein D (cbpD)	10-33,35-41,72-84,129-138,158-163,203-226,243-252,258-264,279-302,322-329,381-386,401-406,414-435	B:4, C:3, D:1, E:7, F:1, G:1, H:2, K:26, M:1	184-385	97, 241
SP2204	ribosomal protein L9	4-9,19-24,41-47,75-85,105-110,113-146	H:3, L:4	45-62	98, 242
SP2216	secreted 45 kd protein - homology to glucan binding protein (GbpB) S.mutant	4-25,52-67,117-124,131-146,173-180,182-191,195-206,215-221,229-236,245-252,258-279,286-291,293-302,314-320,327-336,341-353,355-361,383-389	A:130, B:414, C:450, D:162, E:166, F:284, G:90, H:16, I:4, K:10, L:29, M:11	1-285	99, 243
SP-NRF1	Choline binding protein	14-32,38-50,73-84,93-105,109-114	H:1	40-70	100, 244
ARF0408	Hypothetical protein	5-26	L:3	22-34	101, 245
ARF0441	Hypothetical protein	23-28	H:3	13-39	102, 246
ARF0690	Hypothetical protein	8-14	L:2	21-34	103, 247
ARF0878	Hypothetical protein	4-13,20-29,44-50,59-74	H:3	41-69	104, 248
ARF0921	Hypothetical protein	4-9, 19-42, 48-59, 71-83	M:4	57-91	105, 249
ARF1153	Hypothetical protein	4-14	M:7	10-28	106, 250
ARF1515	Hypothetical protein	22-28,32-42,63-71,81-111,149-156,158-167,172-180,182-203,219-229	G:4, H:5	27-49	107, 251

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
ARF1519	Hypothetical protein	17-27	H:3	23-32	108, 252
ARF1905	Hypothetical protein	18-24	H:2	28-38	109, 253
ARF2044	Hypothetical protein	9-15	G:2; H:5	13-27	110, 254
ARF2155	Hypothetical protein	13-22	H:3	18-29	111, 255
ARF2199	Hypothetical protein	17-26	M:3	2-11	112, 256
CRF0129	Hypothetical protein	4-33	L:4	16-32	113, 257
CRF0200	Hypothetical protein	4-10,37-43,54-84,92-127	H:5, L:1	15-62	114, 258
CRF0236	Hypothetical protein	4-14,20-32,35-60,69-75,79-99,101-109,116-140	L:3	124-136	115, 259
CRF0394	Hypothetical protein	none	H:7	2-13	116, 260
CRF0408	Hypothetical protein	4-13,28-42	L:11	42-57	117, 261
CRF0430	Hypothetical protein	4-14,27-44	G:4, H:8	14-35	118, 262
CRF0498	Hypothetical protein	4-12	H:4	1-27	119, 263
CRF0519	Hypothetical protein	4-18,39-45,47-74	G:5, H:3	35-66	120, 264
CRF0573	Hypothetical protein	8-20,43-77	I:3, L:9	17-36	121, 265
CRF0713	Hypothetical protein	4-30,35-45,51-57	L:3	35-49	122, 266
CRF0722	Hypothetical protein	4-24,49-57	G:18	15-34	123, 267
CRF0764	Hypothetical protein	4-22	L:4	8-27	124, 268
CRF1079	Hypothetical protein	13-25,32-59,66-80	H:5	21-55	125, 269
CRF1248	Hypothetical protein	4-10,24-33,35-42,54-65,72-82,98-108	H:1	15-30	126, 270
CRF1398	Hypothetical protein	8-19	H:1, L:3	17-47	127, 271
CRF1412	Hypothetical protein	12-18,40-46	L:8	31-52	128, 272
CRF1467	Hypothetical protein	4-20,35-78,83-102,109-122	I:4	74-86	129, 273
CRF1484	Hypothetical protein	7-17,21-41,46-63	I:5	2-20	130, 274
CRF1587	Hypothetical protein	30-37	G:3, H:3, L:4	2-33	131, 275
CRF1606	Hypothetical protein	4-13,17-25	L:3	1-15	132, 276
CRF1623	Hypothetical protein	17-31,44-51	M:6	20-51	133, 277
CRF1625	Hypothetical protein	20-30	L:10	5-23	134, 278
CRF1640	Hypothetical protein	13-33,48-71	I:5	92-110	135, 279
CRF1702	Hypothetical protein	4-9,50-69,76-88,96-106,113-118	L:6	12-34	136, 280
CRF1825	Hypothetical protein	4-24	L:11	6-26	137, 281
CRF1883	Hypothetical protein	7-26	H:61, L:77	14-30	138, 282
CRF1991	Hypothetical protein	9-39,46-68,75-82,84-103	H:6, L:2	26-44	139, 283
CRF1992	Hypothetical protein	4-30,33-107	M:7	58-84	140, 284
CRF2004	Hypothetical protein	4-12	L:3	9-51	141, 285
CRF2030	Hypothetical protein	12-18,29-37	H:5, L:1, M:1	6-37	142, 286

S. pneumoniae antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
CRF2065	Hypothetical protein	4-21,33-52,64-71	I:1, M:6	16-37	143, 287
CRF2232	Hypothetical protein	9-19	L:3	2-30	144, 288

Table 2. **Immunogenicity of epitopes in peptide ELISA**

Peptides	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13	N1	N2	N3	N4	N5	N6	N7	N8	N9	N10	S	from	to	Seq ID
ARF0408.1	nd					nd		nd																			
ARF0441.1	nd					nd		nd																15	20	37	245
ARF0690.1	nd					nd		nd																26	8	27	246
ARF0878.1						nd						nd	nd											20	10	27	247
ARF0878.2						nd						nd	nd											22	42	59	248
ARF0921.1						nd						nd	nd											11	52	69	248
ARF0921.2						nd						nd	nd											15	63	80	249
ARF1153.1	nd					nd		nd																14	74	91	249
ARF1515.1	nd					nd		nd																19	11	28	250
ARF1519.1	nd					nd		nd																18	28	49	251
ARF1905.1	nd					nd		nd																15	15	32	252
ARF2044.1	nd					nd		nd																21	4	20	253
ARF2155.1	nd					nd		nd																18	10	27	254
ARF2199.1	nd					nd		nd																15	17	34	255
CRF0129.1	nd					nd		nd																19	1	18	256
CRF0200.1	nd					nd		nd																15	16	33	257
CRF0200.2	nd					nd		nd																12	16	36	258
CRF0200.3	nd					nd		nd																9	30	49	258
CRF0236.1						nd						nd	nd											10	43	62	258
CRF0394.1	nd					nd		nd																19	122	139	259
CRF0408.1	nd					nd		nd																20	1	18	260
CRF0430.1	nd					nd		nd																19	41	58	261
CRF0498.1	nd					nd		nd																15	15	35	262
CRF0573.1						nd						nd	nd											21	2	27	263
CRF0713.1	nd					nd		nd																22	18	36	265
CRF0764.1	nd					nd		nd																20	34	51	266
CRF1079.1	nd					nd		nd																16	9	27	268
CRF1398.1	nd					nd		nd																27	22	47	269
CRF1398.2	nd					nd		nd																24	18	36	271
CRF1412.1						nd						nd	nd											21	29	47	271
CRF1467.1	nd					nd		nd																9	32	52	272
CRF1484.1	nd					nd		nd																11	72	89	273
CRF1587.1	nd					nd		nd																20	3	20	274
CRF1587.2	nd					nd		nd																23	3	21	275
CRF1606.1	nd					nd		nd																21	15	33	275
CRF1625.1	nd					nd		nd																22	1	18	276
CRF1640.1	nd					nd		nd																23	6	23	278
CRF1702.1						nd						nd	nd											18	93	110	279
CRF1825.1	nd					nd		nd																18	13	34	280
CRF1825.2	nd					nd		nd																24	7	26	281
CRF1883.1	nd					nd		nd																24	9	26	281
CRF1991.1	nd					nd		nd																20	16	33	282
CRF1992.1	nd							nd			nd													24	27	44	283
CRF2004.1	nd					nd		nd																19	67	84	284
CRF2004.2	nd					nd		nd																20	10	33	285
CRF2030.1	nd					nd		nd																22	26	50	285
CRF2030.2	nd					nd		nd																21	7	25	286
																								20	19	37	286

CRF2065.1	nd					nd		nd																21	17	37	287
CRF2232.1	nd					nd		nd																23	3	20	288
CRF2232.2	nd					nd		nd																19	13	30	288
SP0008.1											nd	nd	nd											28	62	80	145
SP0008.2											nd	nd	nd											21	75	93	145
SP0069.1						nd						nd	nd											17	92	108	147
SP0071.1	nd					nd		nd					31											15	332	349	148
SP0071.2						nd						nd	nd											13	177	200	148
SP0071.3						nd						nd	nd											4	1755	1777	148
SP0082.1						nd						nd	nd											4	109	133	149
SP0082.2	nd					nd		nd																24	149	174	149
SP0082.3	nd					nd		nd																26	260	285	149
SP0082.4						nd						nd	nd											20	460	485	149
SP0107.1	nd							nd			nd													10	26	47	150
SP0107.2	nd							nd			nd													11	42	64	150
SP0117.1											nd	nd	nd											18	22	41	151
SP0117.2											nd	nd	nd											57	35	54	151
SP0117.3											nd	nd	nd											64	115	130	151
SP0117.4											nd	nd	nd											17	306	325	151
SP0117.5											nd	nd	nd											15	401	420	151
SP0117.6											nd	nd	nd											68	454	478	151
SP0222.1						nd						nd	nd											15	22	45	155
SP0368.1						nd						nd	nd											22	156	174	160
SP0368.2											nd	nd	nd											32	924	940	160
SP0368.2b						nd						nd	nd											12	1485	1496	160
SP0368.3						nd						nd	nd											14	1447	1462	160
SP0368.4						nd						nd	nd											11	1483	1498	160
SP0369.1						nd						nd	nd											16	457	475	161
SP0377.1						nd						nd	nd											11	302	325	163
SP0378.1						nd						nd	nd											17	288	305	164
SP0390.1						nd						nd	nd											11	244	266	165
SP0390.2	nd					nd		nd																24	260	282	165
SP0454.1											nd	nd	nd											64	204	225	166
SP0454.2											nd	nd	nd											38	220	241	166
SP0463.1	nd							nd			nd													20	324	345	167
SP0463.2	nd							nd			nd													26	340	361	167
SP0463.3	nd							nd			nd													19	356	377	167
SP0463.4	nd							nd			nd													9	372	393	167
SP0463.5	nd							nd			nd													13	388	408	167
SP0466.1	nd					nd		nd																22	39	64	168
SP0468.1	nd					nd		nd																21	54	76	169
SP0468.2	nd					nd		nd																24	70	92	169
SP0498.1	nd							nd			nd													13	1227	1247	170
SP0498.2	nd							nd			nd													8	1539	1559	170
SP0498.3	nd							nd			nd													16	1554	1574	170
SP0498.4	nd							nd			nd													13	1569	1589	170
SP0498.5	nd							nd			nd													15	1584	1604	170
SP0498.6	nd							nd			nd													11	1242	1262	170
SP0498.8	nd							nd			nd													24	1272	1292	170
SP0498.9	nd							nd			nd													9	1287	1308	170
SP0498.10	nd							nd			nd													63	1456	1477	170

SP0498.11	nd							nd			nd													59	1472	1494	170
SP0498.12	nd							nd			nd													20	1488	1510	170
SP0498.13	nd							nd			nd													10	1505	1526	170
SP0519.1	nd					nd		nd																25	351	368	172
SP0529.1	nd							nd			nd													6	179	200	173
SP0529.2	nd							nd			nd													23	195	216	173
SP0529.3	nd							nd			nd													7	211	232	173
SP0529.4	nd							nd			nd													8	227	248	173
SP0529.5	nd							nd			nd													18	243	263	173
SP0564.1											nd	nd	nd											63	13	37	174
SP0609.1	nd					nd		nd																16	208	224	175
SP0641.1											nd	nd	nd											34	42	64	177
SP0641.2											nd	nd	nd											61	59	81	177
SP0641.3											nd	nd	nd											0	304	328	177
SP0641.4											nd	nd	nd											36	323	348	177
SP0641.5											nd	nd	nd											76	465	489	177
SP0641.6											nd	nd	nd											64	968	992	177
SP0641.7											nd	nd	nd											52	1399	1418	177
SP0641.8											nd	nd	nd											25	1412	1431	177
SP0641.9	nd					nd		nd																18	2092	2111	177
SP0648.1	nd					nd		nd																11	1528	1547	178
SP0648.2	nd					nd		nd																24	1541	1560	178
SP0664.1	nd					nd		nd																28	184	200	179
SP0664.2	nd					nd		nd																18	367	388	179
SP0664.3	nd					nd		nd																15	382	403	179
SP0664.4	nd					nd		nd																14	409	429	179
SP0664.5	nd					nd		nd																20	425	444	179
SP0664.6	nd					nd		nd																17	438	457	179
SP0667.1	nd							nd			nd													22	27	50	180
SP0667.2	nd							nd			nd													16	45	67	180
SP0749.2	nd					nd		nd																24	114	131	182
SP0770.1	nd					nd		nd																17	405	419	183
SP0785.1	nd							nd			nd													11	113	134	184
SP0785.2	nd							nd			nd													10	129	150	184
SP0785.3	nd							nd			nd													8	145	166	184
SP0785.4	nd							nd			nd													11	161	182	184
SP0785.5	nd							nd			nd													8	177	198	184
SP0930.1	nd					nd		nd																30	495	515	186
SP0943.1	nd					nd		nd																19	346	358	187
SP1004.1	nd					nd		nd																21	208	224	190
SP1154.1	nd					nd		nd																33	178	194	192
SP1154.2	nd					nd		nd																28	202	223	192
SP1154.3	nd					nd		nd																21	217	238	192
SP1154.4	nd					nd		nd																19	288	308	192
SP1154.5	nd					nd		nd																16	1355	1372	192
SP1175.1	nd					nd		nd																56	57	78	194
SP1241.1	nd							nd			nd	48												26	347	369	197
SP1241.2	nd							nd			nd													18	364	386	197
SP1241.3	nd							nd			nd													25	381	403	197
SP1241.4	nd							nd			nd													21	398	420	197
SP1241.5	nd							nd			nd													26	415	437	197

SP1241.6	nd							nd			nd													16	432	452	197
SP1287.1	nd					nd		nd																20	347	372	198
SP1330.1	nd					nd		nd																18	147	163	199
SP1374.1	nd					nd		nd																15	263	288	200
SP1429.1	nd					nd		nd																20	361	377	202
SP1518.1	nd							nd			nd													19	82	104	204
SP1518.2	nd							nd			nd													28	99	121	204
SP1518.3	nd							nd			nd													21	116	138	204
SP1518.4	nd							nd			nd													26	133	155	204
SP1518.5	nd							nd			nd													19	150	171	204
SP1522.1	nd					nd		nd																12	110	130	205
SP1522.2	nd					nd		nd																13	125	145	205
SP1527.1	nd					nd		nd																22	613	631	206
SP1527.2	nd					nd		nd																20	626	644	206
SP1527.3	nd					nd		nd																16	196	213	206
SP1604.1	nd							nd			nd													13	78	100	208
SP1604.2	nd							nd			nd													20	95	117	208
SP1604.3	nd							nd			nd													15	112	134	208
SP1604.4	nd							nd			nd													25	129	151	208
SP1661.1	nd							nd			nd													18	158	180	209
SP1661.2	nd							nd			nd													10	175	197	209
SP1661.3	nd							nd			nd													13	192	214	209
SP1661.4	nd							nd			nd													16	209	231	209
SP1661.5	nd							nd			nd													12	226	248	209
SP1664.1	nd							nd			nd													24	30	50	210
SP1664.2	nd							nd			nd													26	45	65	210
SP1664.3	nd							nd			nd													11	60	79	210
SP1693.1	nd					nd		nd																20	431	455	213
SP1693.2	nd					nd		nd																18	450	474	213
SP1732.1	nd							nd			nd													25	579	601	214
SP1732.2	nd							nd			nd													15	596	618	214
SP1732.3	nd							nd			nd													19	613	635	214
SP1732.4	nd							nd			nd													22	630	653	214
SP1772.1	nd					nd		nd																27	920	927	217
SP1772.1b	nd							nd			nd													12	98	119	217
SP1772.2	nd							nd			nd													20	114	135	217
SP1772.3	nd							nd			nd													11	130	151	217
SP1772.4	nd							nd			nd													30	146	167	217
SP1772.5	nd							nd			nd													19	162	182	217
SP1888.1	nd					nd		nd																16	36	59	219
SP1891.1	nd					nd		nd																14	194	216	220
SP1891.2	nd					nd		nd																12	381	404	220
SP1937.1	nd					nd		nd																20	236	251	221
SP1937.2	nd					nd		nd																26	255	279	221
SP1954.1	nd					nd		nd																15	80	100	222
SP1954.2	nd					nd		nd																14	141	164	222
SP1980.1	nd					nd		nd																18	128	154	223
SP1992.1	nd							nd			nd													20	82	100	224
SP1992.2	nd							nd			nd													23	95	116	224
SP1992.3	nd							nd			nd													20	111	134	224
SP2027.1	nd					nd		nd																12	55	76	227

SP2027.2	nd					nd		nd																16	71	92	227
SP2027.3	nd					nd		nd																21	87	110	227
SP2048.1						nd						nd	nd											21	91	106	229
SP2051.1						nd						nd	nd											25	74	96	230
SP2092.1	nd					nd		nd																22	140	157	231
SP2108.1	nd					nd		nd																13	4	13	233
SP2136.1	nd					nd		nd																5	41	65	236
SP2136.2	nd					nd		nd																32	499	523	236
SP2190.1	nd					nd		nd																13	122	146	239
SP2190.2	nd					nd		nd																29	191	215	239
SP2190.3	nd					nd		nd																26	288	313	239
SP2190.4	nd					nd		nd																36	445	469	239
SP2190.5	nd					nd		nd																24	511	535	239
SP2201.1	nd					nd		nd																34	347	368	241
SP2204.1	nd					nd		nd																16	46	61	242
SP2216.1						nd						nd	nd											16	15	37	243
SP2216.2						nd						nd	nd											28	32	57	243
SP2216.3						nd						nd	nd											14	101	121	243
SP2216.4						nd						nd	nd											31	115	135	243
SP2216.5						nd						nd	nd											22	138	158	243
SP2216.6						nd						nd	nd											12	152	172	243
SP2216.7						nd						nd	nd											46	220	242	243
SP2216.8						nd						nd	nd											12	236	258	243

Table 3: Gene distribution in *S. pneumoniae* strains.

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype 14 strain)*	Homology 0	Seq. ID (DNA, Prot.)
SP0008	hypothetical protein	n.d.	n.d.		1, 145
SP0032	DNA polymerase I (polA)	n.d.	n.d.		2, 146
SP0069	Choline binding protein I	7	0/166#		3, 147
SP0071	immunoglobulin A1 protease (iga-1)	7	0/477#		4, 148
SP0082	Cell wall surface anchor	50	5/385		5, 149
SP0107	LysM domain protein	50	1/173		6, 150
SP0117	pneumococcal surface protein A (pspA)	n.d.	n.d.		7, 151
SP0191	hypothetical protein	n.d.	n.d.		8, 152
SP0197	dihydrofolate synthetase, putative	n.d.	n.d.		9, 153
SP0212	Ribosomal protein L2	50	0/232		10, 154
SP0222	Ribosomal protein S14	n.d.	n.d.		11, 155
SP0239	Conserved hypothetical protein	n.d.	n.d.		12, 156
SP0251	formate acetyltransferase, putative	n.d.	n.d.		13, 157
SP0295	ribosomal protein S9 (rpsI)	50	1/121		14, 158
SP0330	sugar binding transcriptional regulator RegR	n.d.	n.d.		15, 159
SP0368	cell wall surface anchor family protein	46	4/422#		16, 160
SP0369	Penicillin binding protein 1A	50	1/346		17, 161
SP0374	hypothetical protein	n.d.	n.d.		18, 162
SP0377	Choline binding protein C	29	0/114		19, 163
SP0378	choline binding protein J (cbpJ)	50	2/104		20, 164
SP0390	choline binding protein G (cbpG)	50	3/171#		21, 165
SP0454	hypothetical protein	48	1/303#		22, 166
SP0463	cell wall surface anchor family protein	10	0/298#		23, 167
SP0466	sortase, putative	44	4/243#		24, 168
SP0468	Sortase, putative	18	0/254#		25, 169
SP0498	endo-beta-N-acetylglucosaminidase, putative	50	4/334		26, 170
SP0509	type I restriction-modification system, M subunit	n.d.	n.d.		27, 171
SP0519	dnaJ protein (dnaJ)	50	2/312		28, 172
SP0529	BlpC ABC transporter (blpB)	50	6/306		29, 173
SP0564	hypothetical protein	50	1/127		30, 174
SP0609	amino acid ABC transporter, amino	50	0/232		31, 175

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype 14 strain)*	Homology ()	Seq. ID (DNA, Prot.)
	acid-binding pro				
SP0613	metallo-beta-lactamase superfamily protein	n.d.	n.d.		32, 176
SP0641	Serine protease	n.d.	n.d.		33, 177
SP0648	beta-galactosidase (bgaA)	50	0/304		34, 178
SP0664	Zinc metalloprotease ZmpB, putative	n.d.	n.d.		35, 179
SP0667	pneumococcal surface protein, putative	45	18/297		36, 180
SP0688	UDP-N-acetylmuramoylalanine--D-glutamate ligase	n.d.	n.d.		37, 181
SP0749	branched-chain amino acid ABC transporter	50	4/303		38, 182
SP0770	ABC transporter, ATP-binding protein	50	0/307		39, 183
SP0785	conserved hypothetical protein	50	0/304		40, 184
SP0914	nodulin-related protein, truncation	n.d.	n.d.		41, 185
SP0930	choline binding protein E (cbpE)	47	17/294		42, 186
SP0943	Gid protein (gid)	n.d.	n.d.		43, 187
SP0952	alanine dehydrogenase, authentic frameshift (ald)	n.d.	n.d.		44, 188
SP1003	conserved hypothetical protein (PAT)	n.d.	n.d.		45, 189
SP1004	Conserved hypothetical protein	n.d.	n.d.		46, 190
SP1124	glycogen synthase (glgA)	n.d.	n.d.		47, 191
SP1154	IgA1 protease	28	13/470; 80missing		48, 192
SP1174	conserved domain protein (PAT)	n.d.	n.d.		49, 193
SP1175	conserved domain protein	n.d.	n.d.		50, 194
SP1221	type II restriction endonuclease	n.d.	n.d.		51, 195
SP1227	DNA-binding response regulator	n.d.	n.d.		52, 196
SP1241	amino acid ABC transporter, amino acid-binding protein	50	0/285		53, 197
SP1287	signal recognition particle protein (ffh)	49	0/300		54, 198
SP1330	N-acetylmannosamine-6-P epimerase, putative (nanE)	14	0/211#		55, 199
SP1374	Chorismate sythetase (aroC)	50	0/289		56, 200
SP1378	conserved hypothetical protein	n.d.	n.d.		57, 201
SP1429	peptidase, U32 family	50	8/305		58, 202
SP1478	oxidoreductase, aldo/keto reductase family	n.d.	n.d.		59, 203
SP1518	conserved hypothetical protein	50	4/313; 3 additional		60, 204

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype 14 strain)*	Homology ()	Seq. ID (DNA, Prot.)
SP1522	conserved domain protein	n.d.	n.d.		61, 205
SP1527	oligopeptide ABC transporter	50	0/463		62, 206
SP1573	lysozyme (lytC)	n.d.	n.d.		63, 207
SP1604	hypothetical protein	50	3/138		64, 208
SP1661	cell division protein DivIVA	50	3/236		65, 209
SP1664	ylmF protein (ylmF)	50	0/164		66, 210
SP1676	N-acetylneuraminate lyase, putative	n.d.	n.d.		67, 211
SP1687	neuraminidase B (nanB)	n.d.	n.d.		68, 212
SP1693	neuraminidase A (nanA)	n.d.	n.d.		69, 213
SP1732	serine/threonine protein kinase	49	2/293		70, 214
SP1735	methionyl-tRNA formyltransferase (fmt)	n.d.	n.d.		71, 215
SP1759	preprotein translocase, SecA subunit (secA-2)	n.d.	n.d.		72, 216
SP1772	cell wall surface anchor family protein	23	12/253#		73, 217
SP1804	general stress protein 24, putative	n.d.	n.d.		74, 218
SP1888	oligopeptide ABC transporter, ATP-binding protein AmiE	n.d.	n.d.		75, 219
SP1891	oligopeptide ABC transporter,	n.d.	n.d.		76, 220
SP1937	Autolysin (lytA)	50	0/275		77, 221
SP1954	serine protease, subtilase family, authentic frame	12	0/305#		78, 222
SP1980	cmp-binding-factor 1 (cbf1)	n.d.	n.d.		79, 223
SP1992	cell wall surface anchor family protein	50	4/197		80, 224
SP1999	catabolite control protein A (ccpA)	n.d.	n.d.		81, 225
SP2021	glycosyl hydrolase	n.d.	n.d.		82, 226
SP2027	Conserved hypothetical protein	n.d.	n.d.		83, 227
SP2039	conserved hypothetical protein	n.d.	n.d.		84, 228
SP2048	Conserved hypothetical protein	50	8/134		85, 229
SP2051	Conpetence protein CglC	50	8/92		86, 230
SP2092	UTP-glucose-1-phosphate uridylyltransferase (galU)	n.d.	n.d.		87, 231
SP2099	Penecillin binding protein 1B	n.d.	n.d.		88, 232
SP2108	Maltose ABC transporter	50	1/279		89, 233
SP2120	hypothetical protein	n.d.	n.d.		90, 234
SP2128	transketolase, N-terminal subunit	n.d.	n.d.		91, 235
SP2136	choline binding protein PcpA	45	1/382		92, 236

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype 14 strain)*	Homology ()	Seq. ID (DNA, Prot.)
SP2141	glycosyl hydrolase-related protein	n.d.	n.d.		93, 237
SP2180	conserved hypothetical protein	n.d.	n.d.		94, 238
SP2190	choline binding protein A (cbpA)	47	for: 48,8%; rev: 2 /17#		95, 239
SP2194	ATP-dependent Clp protease, ATP-binding subunit	50	1/262		96, 240
SP2201	choline binding protein D (cbpD)	50	7/384		97, 241
SP2204	ribosomal protein L9	n.d.	n.d.		98, 242
SP2216	secreted 45 kd protein - homology to glucan binding protein (GbpB) S.mutant	50	0/347		99, 243
SP-NRF1	Choline binding protein	n.d.	n.d.		100, 244
ARF0408	Hypothetical protein	n.d.	n.d.		101, 245
ARF0441	Hypothetical protein	n.d.	n.d.		102, 246
ARF0690	Hypothetical protein	n.d.	n.d.		103, 247
ARF0878	Hypothetical protein	n.d.	n.d.		104, 248
ARF0921	Hypothetical protein	n.d.	n.d.		105, 249
ARF1153	Hypothetical protein	n.d.	n.d.		106, 250
ARF1515	Hypothetical protein	n.d.	n.d.		107, 251
ARF1519	Hypothetical protein	n.d.	n.d.		108, 252
ARF1905	Hypothetical protein	n.d.	n.d.		109, 253
ARF2044	Hypothetical protein	n.d.	n.d.		110, 254
ARF2155	Hypothetical protein	n.d.	n.d.		111, 255
ARF2199	Hypothetical protein	n.d.	n.d.		112, 256
CRF0129	Hypothetical protein	n.d.	n.d.		113, 257
CRF0200	Hypothetical protein	n.d.	n.d.		114, 258
CRF0236	Hypothetical protein	n.d.	n.d.		115, 259
CRF0394	Hypothetical protein	n.d.	n.d.		116, 260
CRF0408	Hypothetical protein	n.d.	n.d.		117, 261
CRF0430	Hypothetical protein	n.d.	n.d.		118, 262
CRF0498	Hypothetical protein	n.d.	n.d.		119, 263
CRF0519	Hypothetical protein	n.d.	n.d.		120, 264
CRF0573	Hypothetical protein	n.d.	n.d.		121, 265
CRF0713	Hypothetical protein	n.d.	n.d.		122, 266
CRF0722	Hypothetical protein	n.d.	n.d.		123, 267
CRF0764	Hypothetical protein	n.d.	n.d.		124, 268
CRF1079	Hypothetical protein	n.d.	n.d.		125, 269
CRF1248	Hypothetical protein	n.d.	n.d.		126, 270
CRF1398	Hypothetical protein	n.d.	n.d.		127, 271

ORF	Common name	Gene distribution (present of 50)	Amino acid substitutions (in serotype 14 strain)*	Homology ()	Seq. ID (DNA, Prot.)
CRF1412	Hypothetical protein	n.d.	n.d.		128, 272
CRF1467.1	Hypothetical protein	n.d.	n.d.		129, 273
CRF1484	Hypothetical protein	n.d.	n.d.		130, 274
CRF1587	Hypothetical protein	n.d.	n.d.		131, 275
CRF1606	Hypothetical protein	n.d.	n.d.		132, 276
CRF1623	Hypothetical protein	n.d.	n.d.		133, 277
CRF1625	Hypothetical protein	n.d.	n.d.		134, 278
CRF1640	Hypothetical protein	n.d.	n.d.		135, 279
CRF1702	Hypothetical protein	n.d.	n.d.		136, 280
CRF1825	Hypothetical protein	n.d.	n.d.		137, 281
CRF1883	Hypothetical protein	n.d.	n.d.		138, 282
CRF1991	Hypothetical protein	n.d.	n.d.		139, 283
CRF1992	Hypothetical protein	n.d.	n.d.		140, 284
CRF2004	Hypothetical protein	n.d.	n.d.		141, 285
CRF2030	Hypothetical protein	n.d.	n.d.		142, 286
CRF2065	Hypothetical protein	n.d.	n.d.		143, 287
CRF2232	Hypothetical protein	n.d.	n.d.		144, 288

Table 4.

ORF	Common Name	FACS	PK
ARF0878	hypothetical protein	+	nd
ARF0921	hypothetical protein	+	nd
CRF0236	hypothetical protein	++	-
CRF0573	hypothetical protein	+	nd
CRF1412	hypothetical protein	+	nd
CRF1702	hypothetical protein	+	nd
CRF1992	hypothetical protein	++	++
SP0008	hypothetical protein	+	-
SP0069	Choline binding protein I	++	++
SP0082	Cell wall surface anchor	+	-
SP0117	pneumococcal surface protein A (pspA)	+++	+++
SP0212	Ribosomal protein L2	+	++
SP0295	ribosomal protein S9 (rpsl)	++	+++
SP0368	cell wall surface anchor family protein	++	+++
SP0369	Penecillin binding protein 1A	++	++
SP0377	Choline binding protein C	++	++
SP0378	choline binding protein J (cbpJ)	++	nd
SP0390	choline binding protein G (cbpG)	++	+
SP0454	hypothetical protein	++	+++
SP0463	cell wall surface anchor family protein	+	++
SP0466	sortase, putative	++	++
SP0468	Sortase, putative	++	++
SP0519	dnaJ protein (dnaJ)	++	+
SP0609	amino acid ABC transporter, amino acid-bind	++	+
SP0641	Serine protease	+	-
SP0664	Zinc metalloprotease ZmpB	+	++
SP0749	branched-chain amino acid ABC transporter	+	+
SP0770	ABC transporter, ATP-binding protein	++	++
SP1154	IgA1 protease	++	++
SP1287	signal recognition particle protein (ffh)	+	++
SP1330	N-acetylmannoseamine-6-P	++	-
SP1429	peptidase, U32 family	+	++
SP1527	oligopeptide ABC transporter	+	++
SP1759	preprotein translocase, SecA subunit (wrong clone!!!)	+	-
SP1772	cell wall surface anchor family protein	+	+
SP1891	oligopeptide ABC transporter	+	++
SP1937	Autolysin (lytA)	+	-
SP1954	serine protease, subtilase family, auth frame	+	++
SP1980	cmp-binding-factor 1 (cbf1)	+	-
SP2108	Maltose ABC transporter	+	++
SP2136	choline binding protein PcpA	+	++
SP2190	choline binding protein A (cbpA)	+	++
SP2194	ATP-dependent Clp protease, ATP-bind subu	++	++
SP2201	choline binding protein D (cbpD)	+	++
SP2216	secreted 45 kd protein	+	++

Claims:

1. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence, which is selected from the group consisting of:
   a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from **Seq ID No** 1, 101-144.
   b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
   c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
   d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
   e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).

2. The isolated nucleic acid molecule according to claim 1, wherein the sequence identity is at least 80%, preferably at least 95%, especially 100%.

3. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of
   a) a nucleic acid molecule having at least 96% sequence identity to a nucleic acid molecule selected from **Seq ID No** 2-6, 8, 10-16, 18-23, 25-31, 34, 36, 38-42, 44, 47-48, 51, 53, 55-62, 64, 67, 71-76, 78-79, 81-94, 96-100.
   b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
   c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
   d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
   e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

4. An isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of
   a) a nucleic acid molecule selected from **Seq ID No** 9, 17, 24, 32, 37, 43, 52, 54, 65-66, 70, 80,
   b) a nucleic acid molecule which is complementary to the nucleic acid of a),
   c) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

5. The nucleic acid molecule according to any one of the claims 1, 2, 3 or 4, wherein the nucleic acid is DNA.

6. The nucleic acid molecule according to any one of the claims 1,2, 3, 4, or 5 wherein the nucleic acid is RNA.

7. An isolated nucleic acid molecule according to any one of claims 1 to 5, wherein the nucleic acid molecule is isolated from a genomic DNA, especially from a *S. pneumoniae* genomic DNA.

8. A vector comprising a nucleic acid molecule according to any one of claims 1 to 7.

9. A vector according to claim 8, wherein the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragment thereof encoded by the nucleic acid molecule according to any one of claims 1 to 7.

10. ~~A host cell comprising the vector according to claim 8 or 9.~~

11. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 1, 2, 5, 6 or 7 and fragments thereof, wherein the amino acid sequence is selected from the group consisting of **Seq ID No** 145, 245-288.

12. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 3, 5, 6, or 7 and fragments thereof, wherein the amino acid sueqnece is selected from the group consisting of **Seq ID No** 146-150, 152, 154-160, 162-167, 169-175, 178, 180, 182-186, 188, 191-192, 195, 197, 199-206, 208, 211, 215-220, 222-223, 225-238, 240-244.

13. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 4, 5, 6, or 7 and fragments thereof, wherein the amino acid sequence is selected from the group consisting of **Seq ID No** 153, 161, 168, 176, 181, 187, 196, 198, 209-210, 214, 224.

14. Fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 2; the serum reactive epitopes of Table 2, especially peptides comprising amino acid 4-11, 35-64, 66-76, 101-108, 111-119 and 57-114 of **Seq ID No** 145; 5-27, 32-64, 92-102, 107-113, 119-125, 133-139, 148-162, 177-187, 195-201, 207-214, 241-251, 254-269, 285-300, 302-309, 317-324, 332-357, 365-404, 411-425, 443-463, 470-477, 479-487, 506-512, 515-520, 532-547, 556-596, 603-610, 616-622, 624-629, 636-642, 646-665, 667-674, 687-692, 708-720, 734-739, 752-757, 798-820, 824-851, 856-865 and 732-763 of **Seq ID No** 146; 14-21, 36-44, 49-66, 102-127, 162-167, 177-196, 45-109 and 145-172 of **Seq ID No** 147; 17-35, 64-75, 81-92, 100-119, 125-172, 174-183, 214-222, 230-236, 273-282, 287-303, 310-315, 331-340, 392-398, 412-420, 480-505, 515-523, 525-546, 553-575, 592-598, 603-609, 617-625, 631-639, 644-651, 658-670, 681-687, 691-704, 709-716, 731-736, 739-744, 750-763, 774-780, 784-791, 799-805, 809-822, 859-870, 880-885, 907-916, 924-941, 943-949, 973-986, 1010-1016, 1026-1036, 1045-1054, 1057-1062, 1082-1088, 1095-1102, 1109-1120, 1127-1134, 1140-1146, 1152-1159, 1169-1179, 1187-1196, 1243-1251, 1262-1273, 1279-1292, 1306-1312, 1332-1343, 1348-1364, 1379-1390, 1412-1420, 1427-1436, 1458-1468, 1483-1503, 1524-1549, 1574-1588, 1614-1619, 1672-1685, 1697-1707, 1711-1720, 1738-1753, 1781-1787, 1796-1801, 1826-1843, 132-478, 508-592 and 1753-1810 of **Seq ID No** 148; 15-43, 49-55, 71-77, 104-110, 123-130, 162-171, 180-192, 199-205, 219-227, 246-254, 264-270, 279-287, 293-308, 312-322, 330-342, 349-356, 369-377, 384-394, 401-406, 416-422, 432-439, 450-460, 464-474, 482-494, 501-508, 521-529, 536-546, 553-558, 568-574, 584-591, 602-612, 616-626, 634-646, 653-660, 673-681, 688-698, 705-710, 720-726, 736-749, 833-848, 1-199, 200-337, 418-494 and 549-647 of **Seq ID No** 149; 9-30, 65-96, 99-123, 170-178 and 1-128 of **Seq ID No** 150; 7-32, 34-41, 96-106, 127-136, 154-163, 188-199, 207-238, 272-279, 306-312, 318-325, 341-347, 353-360, 387-393, 399-406, 434-440, 452-503, 575-580, 589-601, 615-620, 635-640, 654-660, 674-680, 696-701, 710-731, 1-548 and 660-691 of **Seq ID No** 151; 4-19, 35-44, 48-59, 77-87, 93-99, 106-111, 130-138, 146-161 and 78-84 of **Seq ID No** 152; 24-30, 36-43, 64-86, 93-99, 106-130, 132-145, 148-165, 171-177, 189-220, 230-249, 251-263, 293-300, 302-312, 323-329, 338-356, 369-379, 390-412 and 179-193 of **Seq ID No** 153; 30-39, 61-67, 74-81, 90-120, 123-145, 154-167, 169-179, 182-197, 200-206, 238-244, 267-272 and 230-265 of **Seq ID No** 154; 14-20, 49-65, 77-86 and 2-68 of **Seq ID No** 155; 4-9, 26-35, 42-48, 53-61, 63-85, 90-101, 105-111, 113-121, 129-137, 140-150, 179-188, 199-226, 228-237, 248-255, 259-285, 299-308, 314-331, 337-343, 353-364, 410-421, 436-442 and 110-144 of **Seq ID No** 156; 36-47, 55-63, 94-108, 129-134, 144-158, 173-187, 196-206, 209-238, 251-266, 270-285, 290-295, 300-306, 333-344, 346-354, 366-397, 404-410, 422-435, 439-453, 466-473, 515-523, 529-543, 554-569, 571-585, 590-596, 607-618, 627-643, 690-696, 704-714, 720-728, 741-749, 752-767, 780-799, 225-247 and 480-507 of **Seq ID No** 157; 16-25, 36-70, 80-

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15. A process for producing a *S. pneumoniae* hyperimmune serum reactive antigen or a fragment thereof according to any one of the claims 11 to 14 comprising expressing the nucleic acid molecule according to any one of claims 1 to 7.

16. A process for producing a cell, which expresses a *S. pneumoniae* hyperimmune serum reactive antigen or a fragment thereof according to any one of the claims 11 to 14 comprising transforming or transfecting a suitable host cell with the vector according to claim 8 or claim 9.

17. A pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of claims 11 to 14 or a nucleic acid molecule according to any one of claims 1 to 7.

18. A pharmaceutical composition, especially a vaccine, according to claim 17, characterized in that it further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, neuroactive compounds, especially human growth hormone, alumn, Freund's complete or incomplete adjuvants or combinations thereof.

19. Use of a nucleic acid molecule according to any one of claims 1 to 7 or a hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *S. pneumoniae* infection.

20. An antibody, or at least an effective part thereof, which binds at least to a selective part of the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14.

21. An antibody according to claim 20, wherein the antibody is a monoclonal antibody.

22. An antibody according to claim 20 or 21, wherein said effective part comprises Fab fragments.

23. An antibody according to any one of claims 20 to 22, wherein the antibody is a chimeric antibody.

24. An antibody according to any one of claims 20 to 23, wherein the antibody is a humanized antibody.

25. A hybridoma cell line, which produces an antibody according to any one of claims 20 to 24.

26. A method for producing an antibody according to claim 20, characterized by the following steps:
   - initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 11 to 14, to said animal,
   - removing an antibody containing body fluid from said animal, and
   - producing the antibody by subjecting said antibody containing body fluid to further purification steps.

27. Method for producing an antibody according to claim 21, characterized by the following steps:
    - initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 12 to 15, to said animal,
    - removing the spleen or spleen cells from said animal,
    - producing hybridoma cells of said spleen or spleen cells,
    - selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
    - producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.

28. Use of the antibodies according to any one of claims 20 to 24 for the preparation of a medicament for treating or preventing *S. pneumoniae* infections.

29. An antagonist, which binds to the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14.

30. A method for identifying an antagonist capable of binding to the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 comprising:
    a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment thereof; and
    b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.

31. A method for identifying an antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 to its interaction partner comprising:
    a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to any one of claims 11-14,
    b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to any one of the claims 20 to 24,
    c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form a interaction complex,
    d) providing a candidate antagonist,
    e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex ,
    f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.

32. Use of any of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14 for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.

33. A process for *in vitro* diagnosing a disease related to expression of the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 7 or the presence of the hyperimmune

serum reactive antigen or fragment thereof according to any one of claims 11-14.

34. A process for *in vitro* diagnosis of a bacterial infection, especially a *S. pneumoniae* infection, comprising analysing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 7 or the presence of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14.

35. Use of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14 for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is selected from the group comprising anticalines.

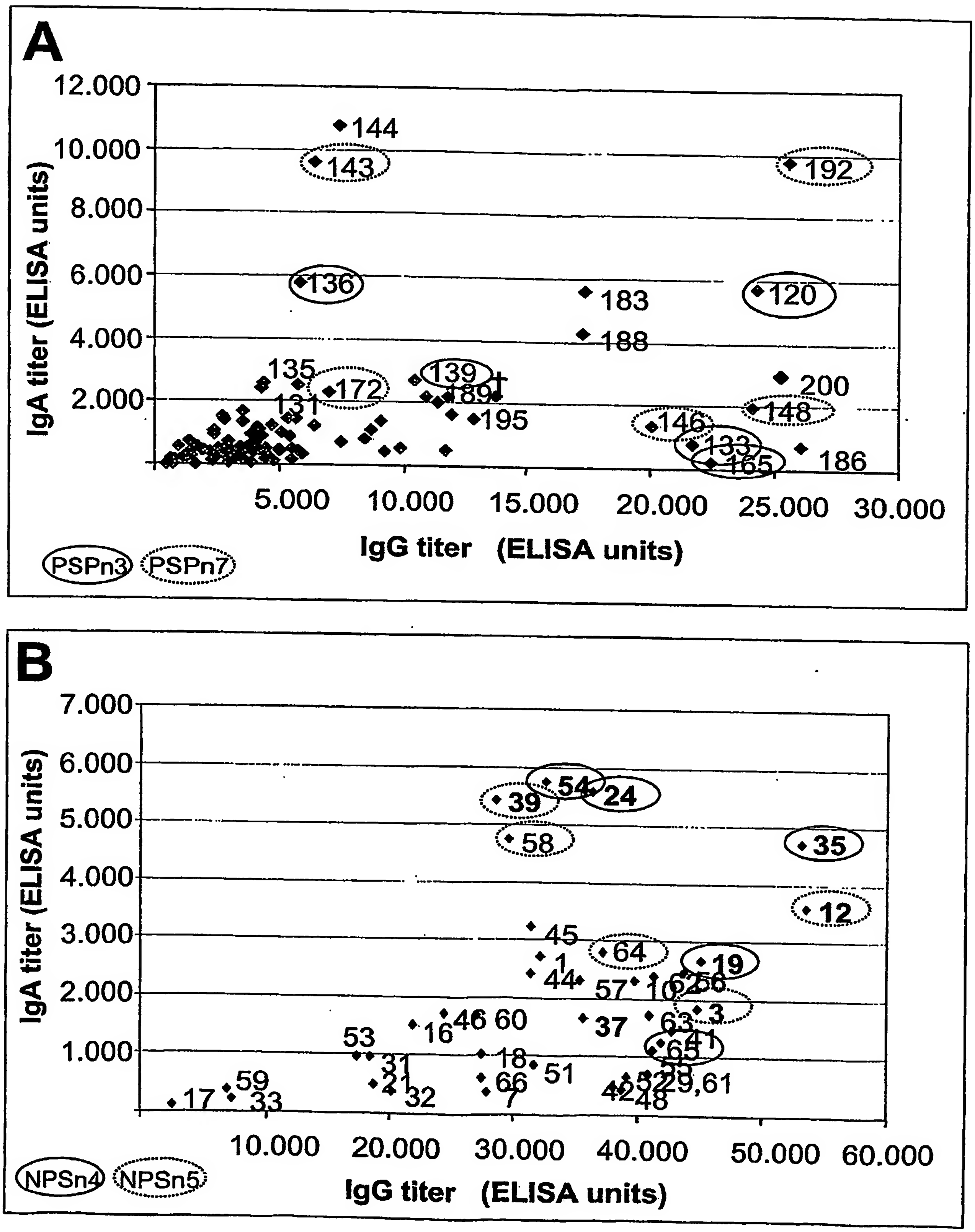
36. Use of the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and spiegelmers.

37. Use of a nucleic acid molecule according to any one of claims 11 to 14 for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

Summary:

S. pneumoniae antigens

The present invention discloses isolated nucleic acid molecules encoding a hyperimmune serum reactive antigen or a fragment thereof as well as hyperimmune serum reactive antigens or fragments thereof from *S. pneumoniae*, methods for isolating such antigens and specific uses thereof.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IgG titer (ELISA units)
PSPn3
PSPn7
B
IgA titer (ELISA units)
IgG titer (ELISA units)
NPSn4
NPSn5

Fig. 1

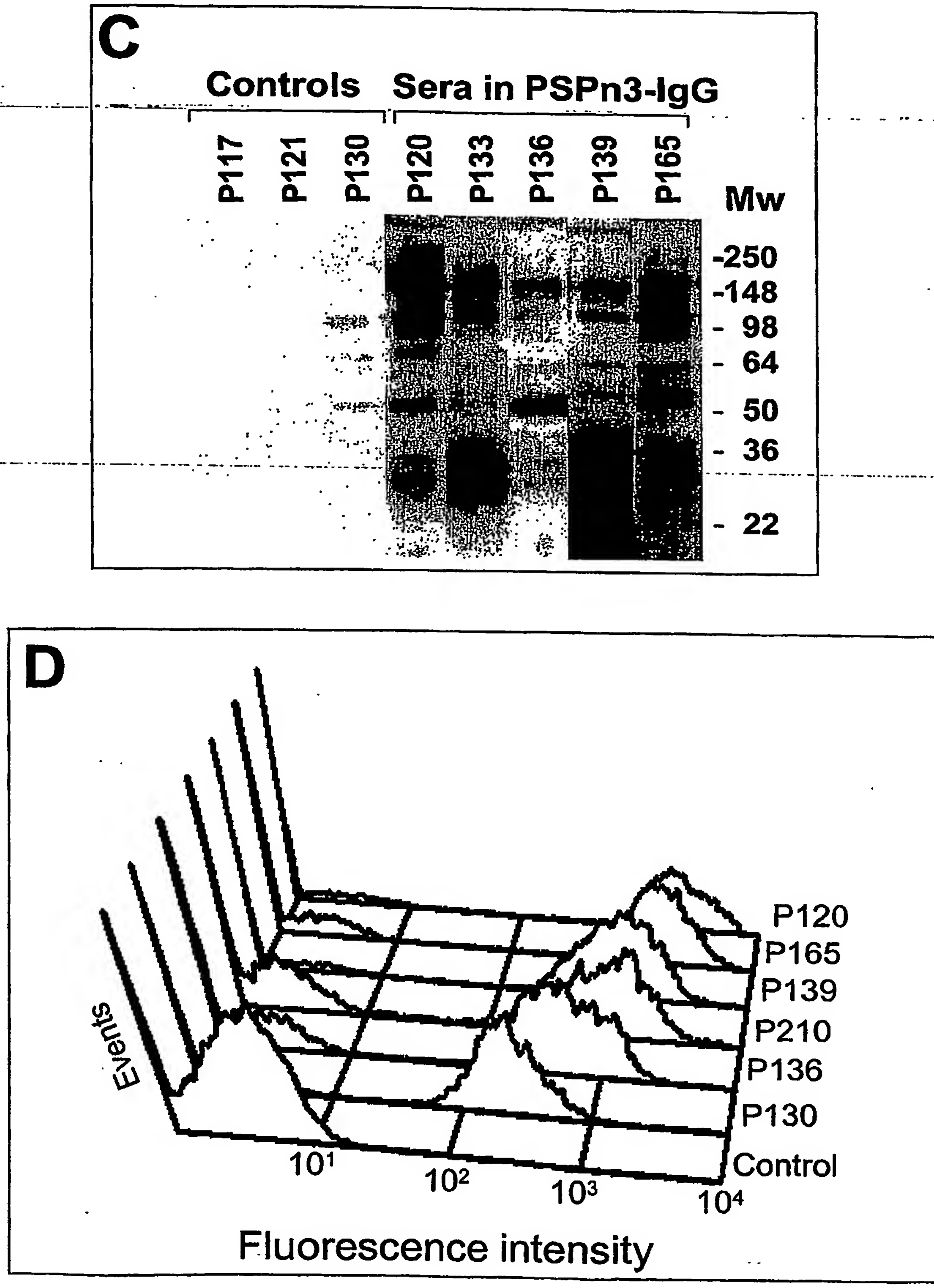

C
Controls
Sera in PSPn3-IgG
P117
P121
P130
P120
P133
P136
P139
P165
Mw
-250
-148
- 98
- 64
- 50
- 36
- 22
D
Events
P120
P165
P139
P210
P136
P130
Control
10¹
10²
10³
10⁴
Fluorescence intensity

Fig.1

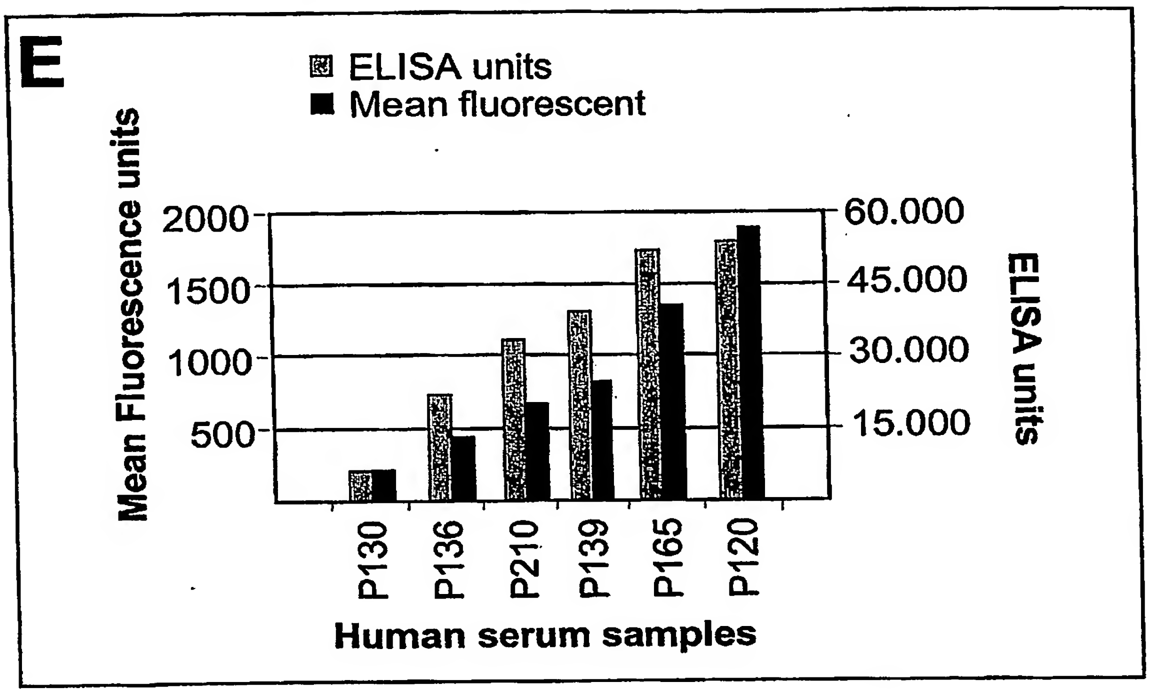
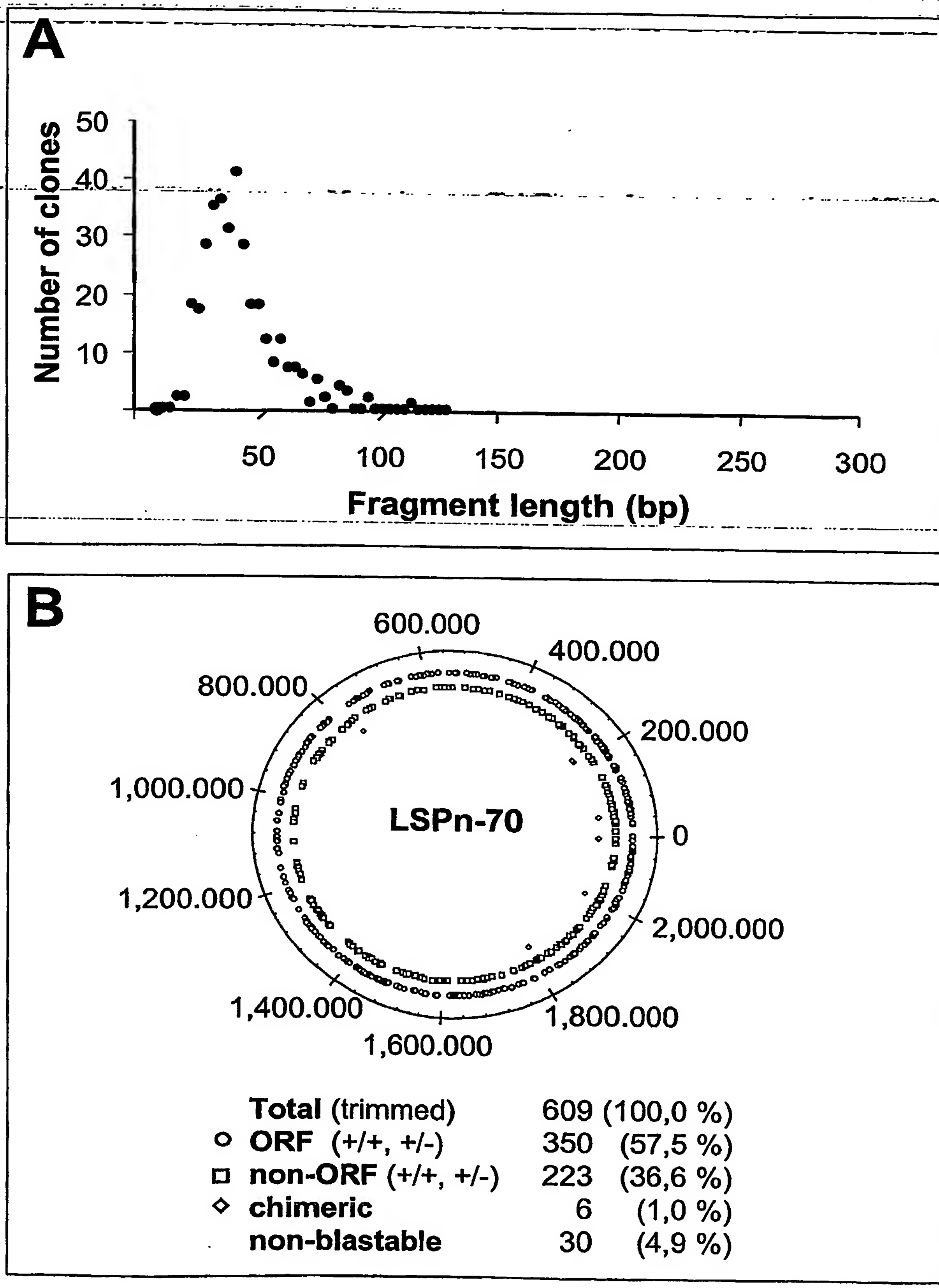

E
ELISA units
Mean fluorescent
Mean Fluorescence units
2000
1500
1000
500
60.000
45.000
30.000
15.000
ELISA units
P130
P136
P210
P139
P165
P120
Human serum samples

Fig.1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40
30
20
10
50
100
150
200
250
300
Fragment length (bp)
B
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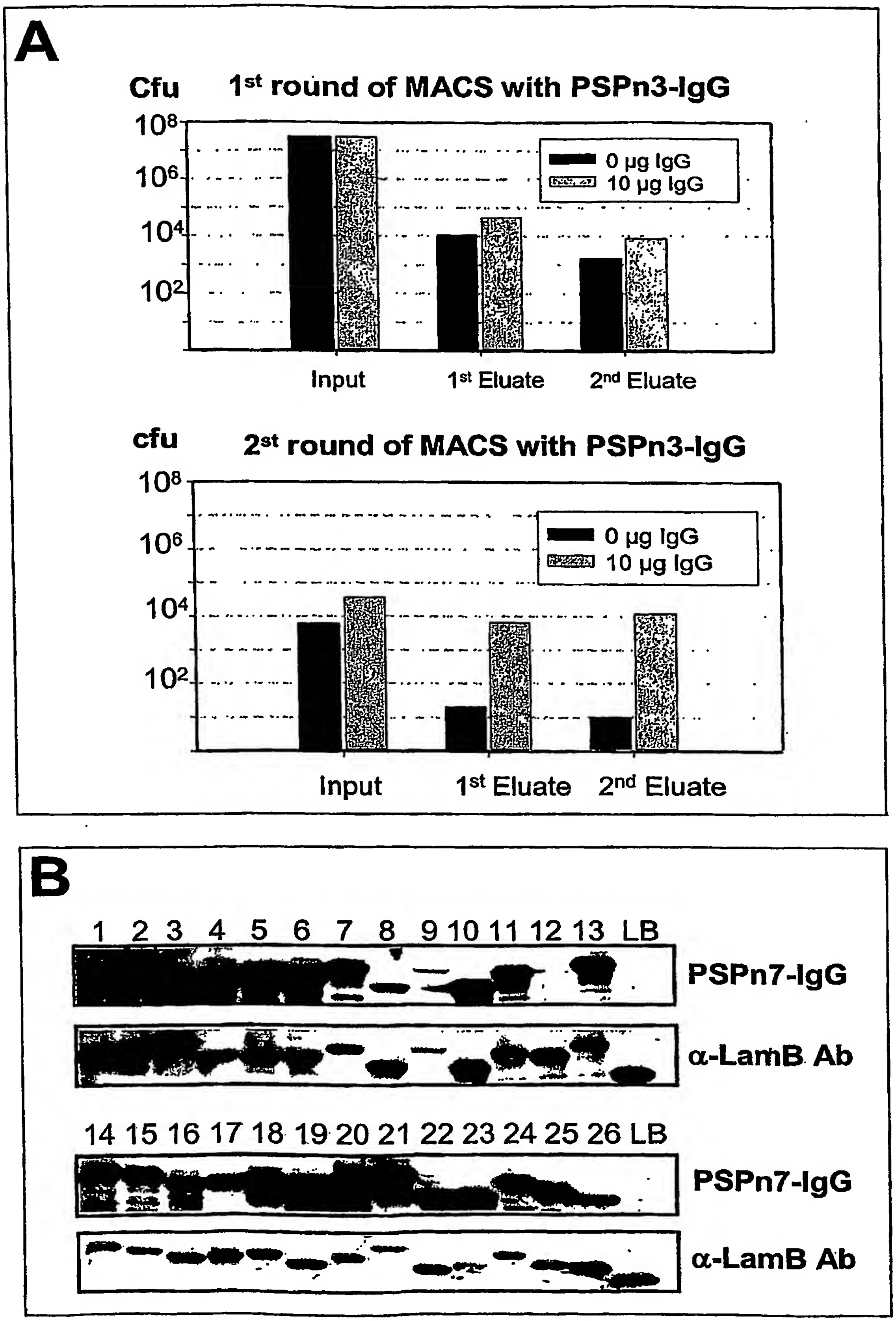
400.000
200.000
0
2,000.000
1,800.000
1,600.000
1,400.000
1,200.000
1,000.000
800.000
LSPn-70
Total (trimmed) 609 (100,0 %)
ORF (+/+, +/-) 350 (57,5 %)
non-ORF (+/+, +/-) 223 (36,6 %)
chimeric 6 (1,0 %)
non-blastable 30 (4,9 %)

Fig. 2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10^6
10^4
10^2
0 µg IgG
10 µg IgG
Input
1st Eluate
2nd Eluate
cfu
2st round of MACS with PSPn3-IgG
10^8
10^6
10^4
10^2
0 µg IgG
10 µg IgG
Input
1st Eluate
2nd Eluate
B
1 2 3 4 5 6 7 8 9 10 11 12 13 LB
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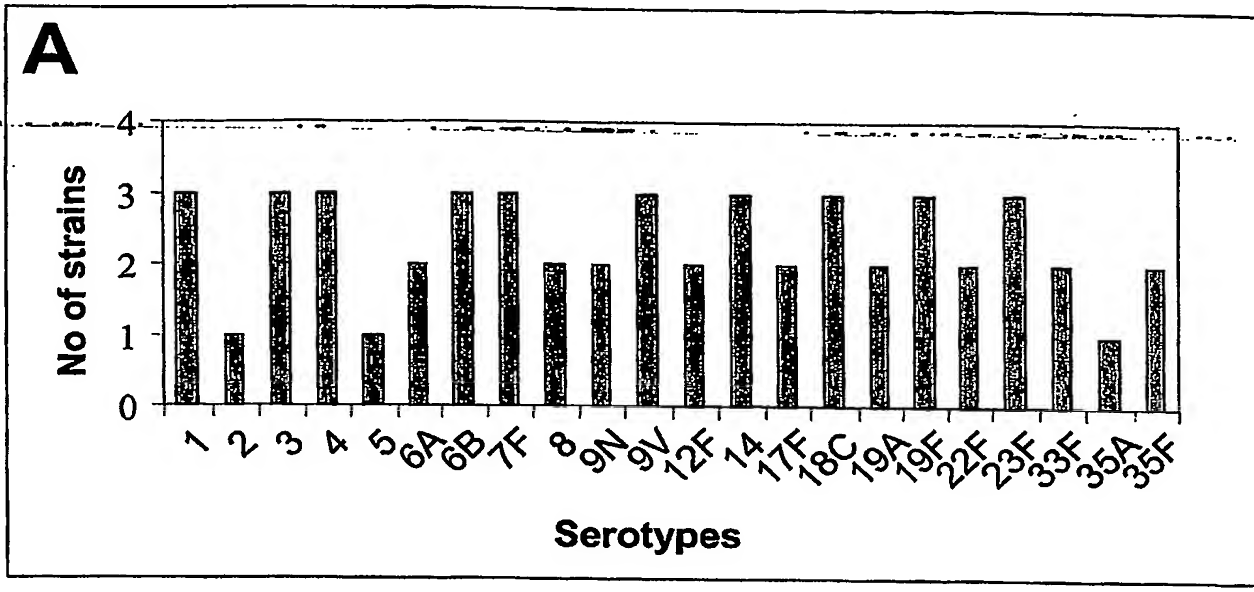
α-LamB Ab
14 15 16 17 18 19 20 21 22 23 24 25 26 LB
PSPn7-IgG
α-LamB Ab

Fig. 3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2
3
4
5
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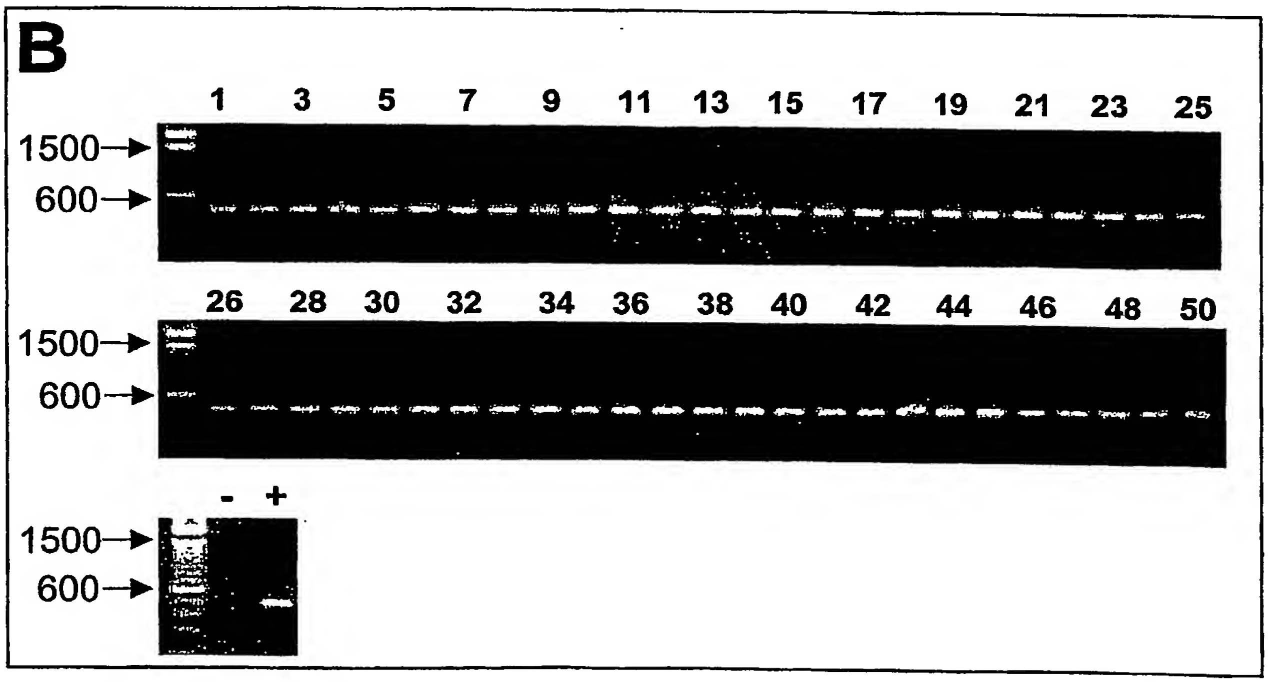
6B
7F
8
9N
9V
12F
14
17F
18C
19A
19F
22F
23F
33F
35A
35F
Serotypes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11
13
15
17
19
21
23
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1500
600
26
28
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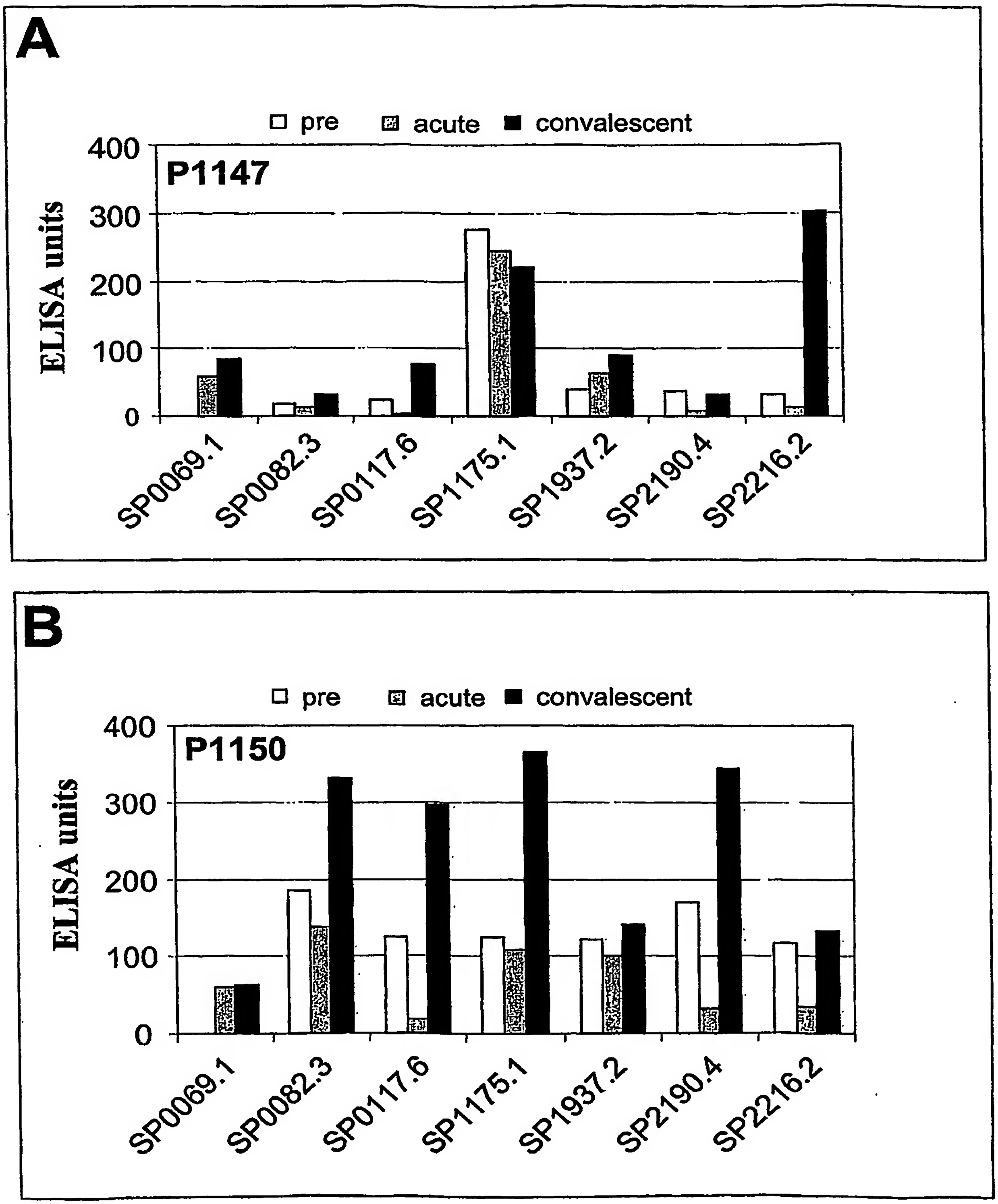
-
+
1500
600

Fig. 4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acute
convalescent
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300
200
100
0
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SP0082.3
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SP1175.1
SP1937.2
SP2190.4
SP2216.2
B
pre
acute
convalescent
400
300
200
100
0
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SP1175.1
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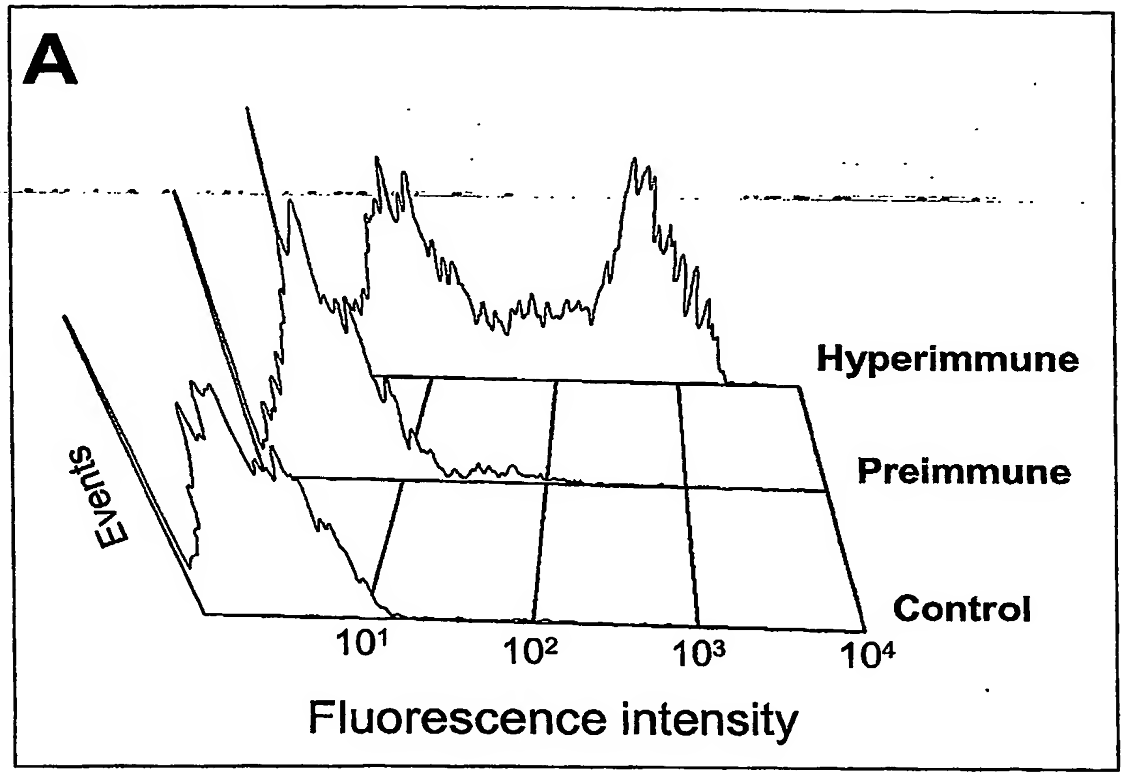
SP2190.4
SP2216.2

Fig. 5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Preimmune
Control
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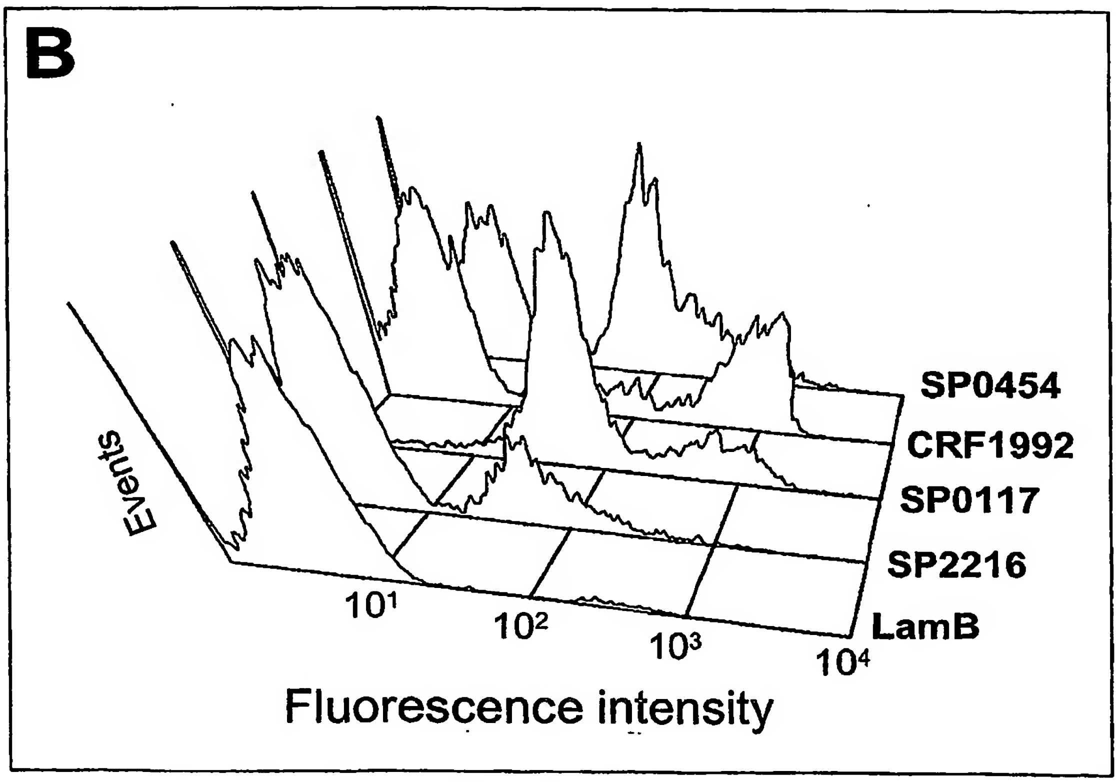
10²
10³
10⁴
Fluorescence intensity


B
Events
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LamB
10¹
10²
10³
10⁴
Fluorescence intensity

Fig. 6

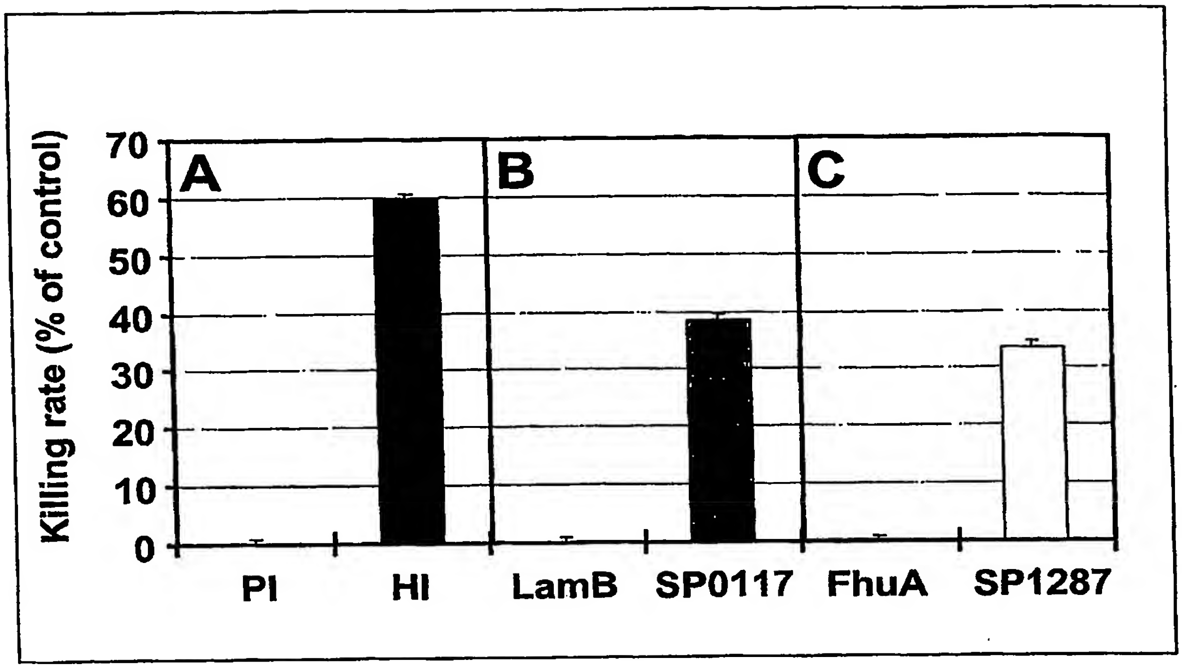
Killing rate (% of control)
70
60
50
40
30
20
10
0
A
B
C
PI
HI
LamB
SP0117
FhuA
SP1287

Fig. 7

SEQUENCE LISTING

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<211> 567

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<213> Streptococcus pneumoniae

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<211> 1248

<212> DNA

<213> Streptococcus pneumoniae

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<211> 831

<212> DNA

<213> Streptococcus pneumoniae

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<211> 267

<212> DNA

<213> Streptococcus pneumoniae

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<213> Streptococcus pneumoniae

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<213> Streptococcus pneumoniae

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<213> Streptococcus pneumoniae

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<212> DNA

<213> Streptococcus pneumoniae

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<213> Streptococcus pneumoniae

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<212> DNA
<213> Streptococcus pneumoniae

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<212> DNA
<213> Streptococcus pneumoniae

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<211> 996
<212> DNA
<213> Streptococcus pneumoniae

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<211> 855

<212> DNA

<213> Streptococcus pneumoniae

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<210> 22
<211> 1890
<212> DNA
<213> Streptococcus pneumoniae

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<210> 23

<211> 1995

<212> DNA

<213> Streptococcus pneumoniae

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<211> 837

<212> DNA

<213> Streptococcus pneumoniae

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<212> DNA

<213> Streptococcus pneumoniae

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cgagggaaa 849

<210> 26

<211> 4977

<212> DNA

<213> Streptococcus pneumoniae

<400> 26

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<213> Streptococcus pneumoniae

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<213> Streptococcus pneumoniae

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<213> Streptococcus pneumoniae

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<211> 762

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<213> Streptococcus pneumoniae

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<212> DNA

<213> Streptococcus pneumoniae

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<211> 6420

<212> DNA

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<211> 996

<212> DNA

<213> Streptococcus pneumoniae

<400> 36

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<213> Streptococcus pneumoniae

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<211> 1158

<212> DNA

<213> Streptococcus pneumoniae

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<211> 1539

<212> DNA

<213> Streptococcus pneumoniae

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<211> 1197

<212> DNA

<213> Streptococcus pneumoniae

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<211> 690

<212> DNA

<213> Streptococcus pneumoniae

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<210> 42

<211> 1881

<212> DNA

<213> Streptococcus pneumoniae

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<211> 1368

<212> DNA

<213> Streptococcus pneumoniae

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<211> 1097

<212> DNA

<213> Streptococcus pneumoniae

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<213> Streptococcus pneumoniae

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<211> 1431

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<213> Streptococcus pneumoniae

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<211> 6012

<212> DNA

<213> Streptococcus pneumoniae

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<210> 49

<211> 2457

<212> DNA

<213> Streptococcus pneumoniae

<400> 49
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<210> 50

<211> 2406

<212> DNA

<213> Streptococcus pneumoniae

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cctgatgagg ttagcaagcg tgaaggaatc aatgctgagc aaatcgtcat caagataaca 180
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<211> 3252

<212> DNA

<213> Streptococcus pneumoniae

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gatgcagctt atacagaaga gcctgataag gggaaaactt tcaaggacca tgatttccac 240
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tttgaaaata at 3252

<210> 52
<211> 702
<212> DNA
<213> Streptococcus pneumoniae

<400> 52
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<210> 53

<211> 2163

<212> DNA

<213> Streptococcus pneumoniae

<400> 53

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<210> 54

<211> 1569

<212> DNA

<213> Streptococcus pneumoniae

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aaacgcaag 1569

<210> 55
<211> 699
<212> DNA
<213> Streptococcus pneumoniae

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aaattggctg attttaatat tccggtaatt gccgaaggaa aaattcatta tccagaacaa 600
ttaaaaaaag cttatagttt aggtgttacc agtgtagtca ttggtggagc gattacacgt 660
ccaaaagaaa ttgctcagcg atttattaat gtcatcaaa 699

<210> 56
<211> 1164
<212> DNA
<213> Streptococcus pneumoniae

<400> 56
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ggtggctacg gtcgtggtgg tcgtatgaag attgagaatg accaggttgt ctttacttcg 180
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caccgagact atacaaagaa ctat 1164

<210> 57

<211> 1170

<212> DNA

<213> Streptococcus pneumoniae

<400> 57
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cgtcagaaat ttacagaaca aattgataaa ggttttgcag gaagaagtta ccagatttta 1080
aacaaatatg gtcttccagc agattttgcc tataataaaa aagatgaaag tagtaattac 1140
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<210> 58

<211> 1284

<212> DNA

<213> Streptococcus pneumoniae

<400> 58
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gacccagcct tgattatgat tgcagtgact gaagcaccag gccttgaaat ccacctttct 360
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gatgttgaaa ttgaagcctt tgtccatgga gctatgtgta tttcatactc tggacgttgt 540
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caatcaggag atatggttcg tgcattaaaa gaaggactca tcaatcttta taaggaagat 1260
ggaaccagcg tcacagttcg agct 1284

<210> 59
<211> 840
<212> DNA
<213> Streptococcus pneumoniae

<400> 59
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cgtcatattg atacggcggc gatttatcag aatgaagaaa gtgttggtca agcaatcaaa 180
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gaaaccttaa aaacgattgc tgttcaatcg ggtgctccac gagttgatga tgtggatttc 840

<210> 60
<211> 1653
<212> DNA
<213> Streptococcus pneumoniae

<400> 60
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attatgagaa aagctcctac cgtgcctact cacccaagtc aaggtgtacc agcttctcca 240
gcagatgaga ttcaaagaga aactcctggt gttccaagtc atccaagtca agatgtacct 300
tcttctccag cggaagaaag tggatcaaga ccaggtccag gtcctgttag acctaagaaa 360

cttgaaagag aatacaatga aaccccaaca agggtagctg tttcctatac gacggcagag 420
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gtagcagatg tcacagaagg caaggtctac tatgctaaca atcaagaaga ccacgaccgc 1620
aatgtcgctg aacatgtcaa cagcaaatta aac 1653

<210> 61

<211> 615

<212> DNA

<213> Streptococcus pneumoniae

<400> 61
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gtcatgaatc tctatgatga gtctgatctg atcagtaata tcaagggtga gtatcgagat 120
aaaaattatt tagaatgggc tcctattgct gaagaaaaac cagtaaaacc gattgaaaag 180
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caaccgacag ctcctttcca aaaggaaaat cctggtgaat ttgtcaaata tagccaaaaa 420
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gaagtgtcag cacctgctcc aaagaaaaac aattatgatt ttctaaagaa gagccaaatc 540
tacaataaaa aaagtaaaca aacagaacaa gaacgtcggg ttgcccaaga gttgaatctg 600
accagaatga cagaa 615

<210> 62

<211> 1956

<212> DNA

<213> Streptococcus pneumoniae

<400> 62

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gcacttgtct caaaatctgc tattgaatat aagaaaaacc ctaattactg ggatgctaag 720
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ttaaccggta caaaaggggt tgaatcatat aaatacctca aagtacaaga taagattgtc 1860
acaacagacg aatatgcaaa agccagagaa aaatggttga aagaaaaaga agaatccaat 1920
aaaaaagccc aagaagaatt ggcaaaacat gtcaaa 1956

<210> 63

<211> 1518

<212> DNA

<213> Streptococcus pneumoniae

<400> 63
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<210> 64

<211> 474

<212> DNA

<213> Streptococcus pneumoniae

<400> 64

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agtattttct ttgtaattgt ggtggtgatg gtcatcgttc tcatctatct atcatcgggg     180
gggagtaatc gcacagcagc cttaaaaggc tttcatgatt ctgatgccag tgtagtacaa     240
atctcatctt caagtagttc tcagcctgag cagagttcag agccagaatc tacttctagt     300
agttcagaag aagctgctaa tcctgaagga acgattaaag ttctcgcagg agaaggggaa     360
gcagctattg ccgctcgtgc aggaatctcc attgctcagt tagaggcctt gaatcctggg     420
cacatggcta caggatcttg gtttgctaat ccaggtgatg ttataaaaat aaaa           474
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<210> 65

<211> 786

<212> DNA

<213> Streptococcus pneumoniae

<400> 65

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cgtgcgaatc atgataaaaa tttgcgtatt aagagtttag aagagcgttt gtcttacttt     180
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aatgctaaga aagtcgctgt tgaaacagaa gaattgaaga acaagagccg tgtcttccac 420
caacgtctca aatctacaat tgagagtcag ttggctattg ttgaatcttc agattgggaa 480
gatattctcc gtccaacagc tacttatctt caaaccagtg atgaagcctt taaagaagtg 540
gttagcgaag tacttggaga accgattcca gctccaattg aagaagaacc aattgatatg 600
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aaagaattgt ctgaatttga agctcagatt aaacaggaag tggaagctcc aactcctgta 720
gtgagtcctc aagttgaaga agagcctctg ctcatccagt tggcccaatg tatgaagaac 780
cagaag 786

<210> 66

<211> 537

<212> DNA

<213> Streptococcus pneumoniae

<400> 66
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gcaggaaacg aaagtatctt gattgatttt cagtatatga cagaggtgca ggctcgtcgt 360
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tctaccatgt atttgttgac accagtgaac gttattgtaa atgttgaaga tatccgttta 480
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<210> 67

<211> 915

<212> DNA

<213> Streptococcus pneumoniae

<400> 67
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aaggagcgct tcctc 915

<210> 68

<211> 2091

<212> DNA

<213> Streptococcus pneumoniae

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<210> 69

<211> 2884

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<213> Streptococcus pneumoniae

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<210> 70

<211> 1977

<212> DNA

<213> Streptococcus pneumoniae

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<210> 71

<211> 933

<212> DNA

<213> Streptococcus pneumoniae

<400> 71

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<210> 72

<211> 2370

<212> DNA

<213> Streptococcus pneumoniae

<400> 72

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<210> 73

<211> 14328

<212> DNA

<213> Streptococcus pneumoniae

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<210> 77

<211> 954

<212> DNA

<213> Streptococcus pneumoniae

<400> 77
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<210> 78

<211> 1401

<212> DNA

<213> Streptococcus pneumoniae

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<210> 79

<211> 924

<212> DNA

<213> Streptococcus pneumoniae

<400> 79
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gggaagctct gggatgccca acctcataac attgaggcct ttaccgcagg taaggttgtc 180
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cgcctgcctc aagctggtga acccaatgac ccagctgatt tcaaggtcaa gtcaccagtt 300
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tccttctata aaccagattt agat 924

<210> 80

<211> 663

<212> DNA

<213> Streptococcus pneumoniae

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gaagctacac cagagtataa gctagaaaat acaccaggtg gagataaggg aggcaatact 120
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cttggtctag tggtggcaac aagtggtttt gctttgctag gaagaaagac tagacgtaga 660
aaa 663

<210> 81

<211> 1008

<212> DNA

<213> Streptococcus pneumoniae

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<210> 82

<211> 1407

<212> DNA

<213> Streptococcus pneumoniae

<400> 82
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catccagaag atttttcga taatgtcgga cctcttgtag ccagtaactt ttttcatact 180
tacaccgaag atttccactt gatgaaggaa attggagtta attctttccg cacttccatc 240
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<211> 408
<212> DNA
<213> Streptococcus pneumoniae

<400> 83
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tacgaaggtg attttgtaaa tggtcaggct gaaggaaaag ggaaactaac aacagaacaa 360
gaagtcgttt atgaaggaac ttttaaacaa ggcgtttttc aacaaaaa 408

<210> 84
<211> 621
<212> DNA
<213> Streptococcus pneumoniae

<400> 84
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aaggttttta cagaactggc caaagccttt caagcaagcc atccagaatg gcaactccaa 180
cagactagcc agtggatgaa tcaggcccag cgtttgagac cacatttttg ggtttatcta 240
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aattcgtctg aagaagaaat cgtagaaggc ttattgaagt cttattctaa aattcttccc 600
tattatctag ctacgagaaa a 621

<210> 85

<211> 459

<212> DNA

<213> Streptococcus pneumoniae

<400> 85
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cagctcctca tttcagaagt tcgctaccag caacaaagcg agcaaaagga gtggctcttg 180

tttgtggacc aacttgaggt agaattagac cgttcgcagt tcgaaaaagt agaaggcaat 240

cgcctataca tgaagcaaga tggcaaggac atcgccatcg gtaagtcaaa gtcagatgat 300

ttccgtaaaa cgaatgctcg tggtcgaggt tatcagccta tggtttatgg actcaaatct 360

gtacggatta cagaggacaa tcaactggtt cgctttcatt tccagttcca aaaaggctta 420

gaaagggagt tcatctatcg tgtggaaaaa gaaaaaagt 459

<210> 86

<211> 324

<212> DNA

<213> Streptococcus pneumoniae

<400> 86
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atgttggtgg tcttgctgat tatcagcgtg cttttcttgc tctttgtacc taatctgacc 120

aagcaaaaag aagcagtcaa tgacaaagga aaagcagctg ttgttaaggt ggtggaaagc 180

caggcagaac tttatagctt agaaaagaat gaagatgcta gcctaagaaa gttacaagca 240

gatggacgca tcacggaaga acaggctaaa gcttataaag aatacaatga taaaaatgga 300

ggagcaaatc gtaaagtcaa tgat 324

<210> 87

<211> 897

<212> DNA

<213> Streptococcus pneumoniae

<400> 87
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<210> 88

<211> 2463

<212> DNA

<213> Streptococcus pneumoniae

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<210> 89

<211> 1269

<212> DNA

<213> Streptococcus pneumoniae

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<210> 90

<211> 465

<212> DNA

<213> Streptococcus pneumoniae

<400> 90
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<210> 91

<211> 855

<212> DNA

<213> Streptococcus pneumoniae

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ttggaggaaa cagaa 855

<210> 92

<211> 1863

<212> DNA

<213> Streptococcus pneumoniae

<400> 92
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<210> 93

<211> 1878

<212> DNA

<213> Streptococcus pneumoniae

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<210> 94

<211> 831

<212> DNA

<213> Streptococcus pneumoniae

<400> 94
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<211> 2079

<212> DNA

<213> Streptococcus pneumoniae

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<211> 2430

<212> DNA

<213> Streptococcus pneumoniae

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<211> 1344

<212> DNA

<213> Streptococcus pneumoniae

<400> 97

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<211> 450

<212> DNA

<213> Streptococcus pneumoniae

<400> 98

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atgattgcag aaggaaaagc aattaaagca caacttgaag cagaagaaac tgttgtagaa 240
tttgttgaaa aagttggtcc agatggtcgt acctttggtt ctattaccaa taagaagatt 300
gcagaagaat tgcaaaagca atttggaatt aagattgata aacgtcatat tcaagtacaa 360
gctccgattc gagcggttgg tttgattgat gtgccagtga aaatctatca agatatcaca 420
agtgtaatca atcttcgtgt gaaagaagga 450

<210> 99

<211> 1176

<212> DNA

<213> Streptococcus pneumoniae

<400> 99

atgaagaaaa aaatcttagc gtcactttta ttaagtacag taatggtttc tcaagtagct 60
gttttaacaa ctgcgcatgc agaaacgact gatgacaaaa ttgctgctca agataataaa 120
attagtaact taacagcaca acaacaagaa gcccaaaaac aagttgacca aattcaggag 180
caagtatcag ctattcaagc tgagcagtct aacttgcaag ctgaaaatga tagattacaa 240
gcagaatcta agaaactcga gggtgagatt acagaacttt ctaaaaacat tgtttctcgt 300
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tatggtcacg tagcggttgt tacagctgtt gaatcaacaa cacgtatcca agtatcagaa 1080

tcaaattatg caggtaatcg tacaattgga aatcaccgtg gatggttcaa tccaacaaca 1140

acttctgaag gttttgttac atatatttat gcagat 1176

<210> 100

<211> 387

<212> DNA

<213> Streptococcus pneumoniae

<400> 100

atggtaaaaa gacgtataag gagagggacg agagaacctg aaaaagttgt tgttcctgag 60

caatcatcta ttccttcgta tcctgtatct gttacatcta accaaggaac agatgtagca 120

gtagaaccag ctaaagcagt tgctccaaca acagactgga aacaagaaaa tggtatgtgg 180

tatttttata atactgatgg ttccatggca acaggttggg tacaagttaa tagttcatgg 240

tactacctca acagcaacgg ttctatgaaa gtcaatcaat ggttccaagt tggtggtaaa 300

tggtattatg taaatacatc gggtgagtta gcggtcaata caagtataga tggctataga 360

gtcaatgata atggtgaatg ggtgcgt 387

<210> 101

<211> 138

<212> DNA

<213> Streptococcus pneumoniae

<400> 101

gagttgcgac ggctatcaag gttggtggac caggagctct attttggatg tggatggcgg 60

ctttctttgg aatggctacc aagtatgcgg aaggactctt ggccatcaaa taccgcacca 120

aggacgacca tggtgcag 138

<210> 102

<211> 93

<212> DNA

<213> Streptococcus pneumoniae

<400> 102

gactgtatca ggaaacaacc gttcacacgc gatgaaccaa acaaaacgtg ccgtaaaacc 60

aaaccttcaa aaagttactg ttcttatcga tgg 93

<210> 103

<211> 78

<212> DNA

<213> Streptococcus pneumoniae

<400> 103
ggacaaagaa accctcgaag aattgaaaga gttatcagaa tggcagaaac gaaaccaaga 60

atatctaaaa aagaaggc 78

<210> 104

<211> 249

<212> DNA

<213> Streptococcus pneumoniae

<400> 104
cagaggaagc tgttcaaaat cttccaccta ttccagaaga aaagtgggtg gaaccagaaa 60

tcatcctgcc tcaagctgaa cttaaattcc ctgaacagga agatgactca gatgacgaag 120

atgttcaggt cgatttttca gccaaagaag cccttgaata caaacttcca agcttacaac 180

tctttgcacc agataaacca aaagatcagt ctaaagagaa gaaaattgtc agagaaaata 240

tcaaaatct 249

<210> 105

<211> 312

<212> DNA

<213> Streptococcus pneumoniae

<400> 105
ttggtgatta tagttttgaa aatccagtcc aaatcggaga cagactttat tttcaagaca 60

tggccattta ttcttttgtc aaaaataata cctttaatgg tattggattg ccaagtctct 120

atctcatgga cgaacaggga gactgtagct tactcaaagc ttttggctat caagacttta 180

aagggagatt atcatgatgg acagtccaaa aaaattaggc tatcacatgc cagcagagta 240

cgaaccccat catggtaccc tcatgatatg gccgactcga ccaggatcat ggccttttca 300

aggaaaggct gc 312

<210> 106

<211> 90

<212> DNA

<213> Streptococcus pneumoniae

<400> 106
gagagactac cagcttttcc tagaagtctt tcagggagga agttggacca aggcggaacc 60
aaagaaaaag gctcggatgg aagaagtcct 90

<210> 107
<211> 912
<212> DNA
<213> Streptococcus pneumoniae

<400> 107
agaaattgcc tctctacttg gaaaagctcc tcaaactatc acactgaaat caagcgtggg 60
acagtccgac aatgtcttgg aaaagggcgc ttcaaagagg tttattctgc cgactacgct 120
caacagtctt atgaaaacaa tcgcaagcgc tcggtcaaga aatcaagctt gaccaaggaa 180
ctaaaggaaa agattctcca ctatcataac caaaaatttt cgcctgaaat gatggttatg 240
gctaaagggg ttaacgtggg aatttcaacc atttactatt ggattcatca tggaaaattg 300
gggttaagca agcaggattt gctttaccct agaaaaggaa aagcgcttaa gaaacaggct 360
agcaccaact ttaaacctgc tggtcaatcc atcgaacagc ggcctgaagc tatcaatctt 420
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tccatcacgg cagataatgg aacggaattc aatcgcttgt ttgatatatt ttctgaggag 660
cacatctatt atgcgcaccc ctatgcctct tgggaaaggg gaactaatga gaatcacaac 720
aggctcattc gtagatagtt acctaaggga accaagaaaa tgactcccaa agaagtcgca 780
ttcatcgaaa agtggattaa caactatcct aaaaaatgct tggactacaa gtcacccaga 840
gaagacttct ggatggctaa cttgaacttg aaatttagca aaatggaaat aatttttatt 900
aaacgcttcc aa 912

<210> 108
<211> 108
<212> DNA
<213> Streptococcus pneumoniae

<400> 108
cctgtcatga ctatctcatc gcctactatg aaaaacatgg atttgtcaac gaaggccagt 60
cccagtcaac ctttgcaggg gaaacatggt atgatatggt ctgggaaa 108

<210> 109

<211> 84

<212> DNA

<213> Streptococcus pneumoniae

<400> 109
acatcatcaa taaggataca cacaaggaaa tcatcgccaa actggactac gacgccccat 60

cttgccctga gtgcggaaac caat 84

<210> 110

<211> 81

<212> DNA

<213> Streptococcus pneumoniae

<400> 110
tacttccttc cacacaagta tgccagagaa agcttatcgc taccctctac caacaaaata 60

ttacacagaa aacaaggttc g 81

<210> 111

<211> 159

<212> DNA

<213> Streptococcus pneumoniae

<400> 111
gcagccttca aaaaagatca aattaatgag cgtgtcgaga aattaggtaa gttaaaacct 60

attacaataa attacaacgg aaaatcagaa gtaattgata gtaaagaaaa attacaagag 120

cttatgaata aagccgttaa agacgaagtg gctcaaata 159

<210> 112

<211> 99

<212> DNA

<213> Streptococcus pneumoniae

<400> 112
gcttatgcgc attctaaaag aagcgctgga agtggcaggg caggaggcag acaatgtctt 60

tgccaatgtc aaaataaatg taggagagat tttaagtat 99

<210> 113

<211> 108

<212> DNA

<213> Streptococcus pneumoniae

<400> 113
cacggccgac cttatcataa gcctcaccaa ccgcatcatc acgggtttcc ccaacaatct 60

tataatctcc tgcctccgaa acataaacca actctgtgtg tccgccgc 108

<210> 114

<211> 390

<212> DNA

<213> Streptococcus pneumoniae

<400> 114
aaaggaaaaa tcctcctgct accaaggcta accactcaaa gatggcaaag aaaaatccgc 60

cctgactcac gtaagtcagc aaataataaa gcaaaccttg acttccataa tagtcgctgt 120

aaatcttccc tgtctgatga agcgcccaac ctgcataaaa atcctgcact tcttgtgcac 180

tcattaagtc gagtaatagc ggtactccta gagttatccc cgttacaagc gtactccata 240

gtaaaatttt caccaaagga agacgacttg attcacgatg atgcgattct tgttcgattt 300

ggtattctag aggttcacga ttctccttat gaacttcttc tactctacca tacacactca 360

tatcgtttct cctgttcaat ttatctgtct 390

<210> 115

<211> 432

<212> DNA

<213> Streptococcus pneumoniae

<400> 115
tttacggtaa gccatgtatt cctcctttat ttatctttta atccaagacc caaatcaatg 60

agtttgagtt tcacttcttc caaactcttg cgtccaagat ttcgtacttt catcatctct 120

gcttcagatt tttctgtcaa atcatgcaca gtattgatac cggcacgttt taaacagttg 180

tatgaacgca cagacaagtc cagttcctca atcgtacgat ctaaaatacg gtcgtcagat 240

tcagtatcag cttctttcat cacttcagtt gacttagcaa tctcagtaag atttgtaaac 300

aaatcaagat gttctgtcaa aatacgtgct gaaagcccta aagcatcttc tggaataatt 360

gttccatttg tcaagatttc aagggttaat ttgtcgaaac catcattgct acctacacga 420

gcaggttcca ct 432

<210> 116

<211> 54

<212> DNA

<213> Streptococcus pneumoniae

<400> 116
cttgtctgca tgaagaataa gggctgctac aaggaaagaa acaactgctg ccac 54

<210> 117

<211> 174

<212> DNA

<213> Streptococcus pneumoniae

<400> 117
ttccattatt tgtcaaaata ctttttagtt tcagcaataa cgactggcga caagaccaag 60

agggcaatca agtttggcag agccatcaag gcgttaacga tatctgcgat aatccagacc 120

atatccaact cgataaatcc tcctaacaag accatgagca caaaaaccac acgg 174

<210> 118

<211> 141

<212> DNA

<213> Streptococcus pneumoniae

<400> 118
ggaaagaagg tattcataaa ataccctcta tcaagagtct cctcaaaaac aggaccgatg 60

attacaggca ggacaaaaga taagatagtc gataaaaagg ttggttgtcc atttgaaaaa 120

agcacggtaa aatactcatc a 141

<210> 119

<211> 111

<212> DNA

<213> Streptococcus pneumoniae

<400> 119
tcttcaccag tttttcctaa acttgtaatg gtatctgggg caaataaacc aagagaaagg 60

cgcaatttcc cattttcgtc taaaatgtca ttccacttaa cctttgtctt g 111

<210> 120

<211> 231

<212> DNA

<213> Streptococcus pneumoniae

<400> 120
tacttaactt ccttctcagt tccgaagata gcttcttcaa aggtcaaatt gacacgatac 60

tggagatcat ctccttggcg aggagcgttt ggattgcgcg aagaaccgcc tccgccgaag 120

aaacttgaga aaatatcctc aaaaccaccg aagccacctg ccccattgaa accgccgaaa 180

ccaccagctc caccaaaacc accattggcg cctgcagcac catactggtc a 231

<210> 121

<211> 267

<212> DNA

<213> Streptococcus pneumoniae

<400> 121
cagtcatggc gtcctattcc agattcaaaa tgctatacac aagaaaaact cactatcccc 60

attaaaagaa gaaaagacat caaggacttc taccacaatt ccatccaaag acacaaaaac 120

agccataaga gtcacctcct tgattcctat aggctgatta taacaagact ggctgaaatt 180

gtacatgaaa ataaaatcct aatagtactc attttgtatg tgactaatat tccgtctcgc 240

tccagaaggt acgaagtaaa tagagtt 267

<210> 122

<211> 180

<212> DNA

<213> Streptococcus pneumoniae

<400> 122
ctgtttcgtt tttatcgtgt aattgttctt tatcgaggtt ggcatattta tcttttaatt 60

cttgtgaatt tgcagtacgt tcaaaacgtt ttccgaaagg atcgattcct tgttcgcgga 120

gcgcagccat tttttcacgg cgaacgatct gctggtcatt tagttcttcc atatgttctg 180

<210> 123

<211> 180

<212> DNA

<213> Streptococcus pneumoniae

<400> 123
ataactcacc ctccactaaa ccctgagcat tttgtttcaa gagtcttttc atctcttggt 60
ttgaagtctt atcagccaaa agatgataga tttctgagaa agccttcaga tagtaggcat 120
cctgaatcag gtaatagcgg aaaatggcag gttctaaatt cccctcttgt aattgtaaaa 180

<210> 124
<211> 90
<212> DNA
<213> Streptococcus pneumoniae

<400> 124
acattggcta aagcagtcgg tttgatgtat tctccaccaa ttccaccaaa accattctta 60
ggccgaataa cgacagattc gtcttctata 90

<210> 125
<211> 249
<212> DNA
<213> Streptococcus pneumoniae

<400> 125
cctggttctc cattttcaga gatttccggt gcaggatttt ttggtgtcgc gaaacgaata 60
tttccacgtc caccacgacc accgtgggca acgataaatt cttgcccatg ttcaatcaaa 120
tctgttaaaa ccttgccagt ctccgcatca cgaacagtcg taccttgtgg tactcgaact 180
ctaaggtcct cagcaccacg accatgcatc cctttggtca tcccttttc accagaatca 240
gccttgaaa 249

<210> 126
<211> 333
<212> DNA
<213> Streptococcus pneumoniae

<400> 126
ataaattcct tgaccttggc cacatcctta tccaaaagaa gggcaccaag aaaggcttca 60
aaggcatcac caagaatggt gtcacgattg cgaccacctg atttttcttc ccctttaccc 120
aacttgataa actggtcaaa ctggcaatca cgcgcaaaac cagctaaact ctcctcacgg 180
acaatcatag cacggagttt tgataggtca ccttcaggct tttaggata ttttttatat 240
agatattctg aaatcaataa ctgtagaaca gcgtctccta aaaattccaa gcgttcattg 300

tgtgaaattt ttaagaggcg gtgctcattg gca 333

<210> 127

<211> 147

<212> DNA

<213> Streptococcus pneumoniae

<400> 127
ccaataggaa aaaggaattg taaagctgaa tgccaatccc accacctgct tgaaaagcag 60

aagaccttcc agtcaagaaa gaccaagaga tatggggcaa gccccgaacc aagatataga 120

gaatcaagga agccaagatt gtcacaa 147

<210> 128

<211> 174

<212> DNA

<213> Streptococcus pneumoniae

<400> 128
cagccattgg gacactcgaa agccgaagaa catgagacta tctgttcgca taccttcgat 60

aaccatacga ccgaaaccat accaaatcaa gtaaaaggcc gtgatatgac ctcgtctgag 120

actcttccat ttccgtctaa aaatcagaat caaggcaaag ccaagcagat tcca 174

<210> 129

<211> 375

<212> DNA

<213> Streptococcus pneumoniae

<400> 129
ccttgctctt tacctgatta tgggctggtt ggttctggct atcattcctg ccattatcag 60

tcaaacgaca cccgttttct ggagtctcat ggtaactggc ggactctgtt atacagttgg 120

agctggattt tatgccaaga aaaaacctta tttccacatg atttggcatc tctttatcct 180

agctgcgtcc gcacttcaat acatcgctat tgtttattac atgtaaaaaa gttgagaaat 240

tcaatctcaa ctttttttctt tacacatatt gataaagtac tggtgcaagc gcacatcatc 300

agtcaattct ggatgaaaag aacttaccaa catatttttt tcttgggctg caacaatttg 360

attgttcact gttgc 375

<210> 130

<211> 207

<212> DNA

<213> Streptococcus pneumoniae

<400> 130
cgagtaaaag ataatcatct ggataagctt gtgaaagctc ttctaaaaag gcgttcatcc 60

actcagtatt acatccacca gctattaaga aaaatgattc gcctgtatgg gcatcaacag 120

ctccataaca atagcgaaat tctcgtatat agtgactatg gacatgtgga cctactccta 180

ttggagacca acaagatccc agtttac 207

<210> 131

<211> 120

<212> DNA

<213> Streptococcus pneumoniae

<400> 131
caagtcatca aaatagacat agcaactaca aataaaacgg aatctgtaaa gagccaaagt 60

gagagagaaa agaaaagatt gacaagcagt aatatactaa aggttagagg gcgaccgata 120

<210> 132

<211> 96

<212> DNA

<213> Streptococcus pneumoniae

<400> 132
gcctttaaga gttccaaggt cccatcactt gatccatcat cgacaaagac atactcgatt 60

tctgtttcca aatctggaag taaagcttcc agagcc 96

<210> 133

<211> 207

<212> DNA

<213> Streptococcus pneumoniae

<400> 133
gataaaactg acccactggc taggaaactt cctgacaaaa gtaagccgtc aacttccttt 60

tgcaccaaat cactttctcc cgttaacatg gcttcattga cttccgcaaa gccttccaaa 120

accaaggcat cactaggaat ctgctctcct gcagacaaac gaatgacatc tcctagcact 180

aattcttcag gattaagagc aacttcc 207

<210> 134

<211> 114

<212> DNA

<213> Streptococcus pneumoniae

<400> 134
ttatgccgat tacaaacaca agcaaggcca cgagggtctg tgaccaatct aacgaagcaa 60

aataaggtat atagatacct aaattatctc cgccagacgc aattgtcagc aatg 114

<210> 135

<211> 330

<212> DNA

<213> Streptococcus pneumoniae

<400> 135
tgcattcaaa gcattggcaa tgagggacag tgcaaaggca atagttgtta cgtaggcaag 60

gagattcatc ttgcccccat atccgatata gttggtcaca aaggcaaaga ggaaggcgat 120

gatggaaatg atgatggccg ccaattttac ctgtttttgg ctcatttggt tgggtctgcc 180

ttcttgcgaa gcttcccact tctttatagc aaaggtataa atgaggaagg tgacgggata 240

ggtaatgatg gccgccttat ttccaaggat ataatcaata gcaccggaca aaatggtatt 300

aacaatacca aagtaatttc cccatttgct 330

<210> 136

<211> 363

<212> DNA

<213> Streptococcus pneumoniae

<400> 136
acgtccacga agctggttat cgatacgacg actttcatga cgttctgtac caataacaca 60

aagtcctcca agttcacgaa caccttcacc aagcttgatg tcggtaccac gacccgccat 120

gttggttgcg atggtaacgg caccacgttg accagcattc atgatgattt gggcttctct 180

atagtggttt ttggcattca agacttcgtg aggaacacca gctgcaacca atttcttaga 240

aatgtagtca ctagtttcaa ccgctactgt accaaccaag acaggttgac ccttttggta 300

acgagcctta acgtcttcga caaccgcttt aaacttagat tcgatacttg cataaagaag 360

gtc 363

<210> 137

<211> 81

<212> DNA

<213> Streptococcus pneumoniae

<400> 137
atctctactg gtgtaccgac ctgttcgatg tatccattgt taaagactgc aattctatca 60

gataaagtca aggcttcctc t 81

<210> 138

<211> 102

<212> DNA

<213> Streptococcus pneumoniae

<400> 138
ttaagtacca tgtccagcat aaagtcaatc ttgtgctctt taccgacaca caccattttc 60

tcaaaatcag ccatatcacc aaaaagagga tccactgcca ta 102

<210> 139

<211> 333

<212> DNA

<213> Streptococcus pneumoniae

<400> 139
agctgctcat actcatctac caactccaag gcatgctcaa tcgtcggttt atcaaaacca 60

acaatattca tctgtgtcac acccatctca gcagccaagg caatttcttc tgcctcacga 120

cctgcaaatt cttctacatt caagtgtgta tgtgtatcaa aaatcatctc ttctaacctc 180

gttttctatc ttctattata ccaaaaaaga ggaggggcac ctaatttttc ggtttcccct 240

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tccacagtta gagacagaag agattggcta cat 333

<210> 140

<211> 330

<212> DNA

<213> Streptococcus pneumoniae

<400> 140
gtaacatctt gcattgttcc tgcagttgct tgcggtgcac ttgttgtctt aggagcagca 60

ttaggagcca ctggtctctt aggaactgta accatggcaa tggcttgcac tccaatcgtt 120
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ttttctgctt ccactcttgc taaaagttct gctttttctt tatcagaaag cggtgcgcct 240
ttgatttcat cctgcttgtc cttggctgct ttttcaatgg catttttagc tgattctttt 300
tcagtagcta attgcttaga agcttgtgat 330

<210> 141
<211> 159
<212> DNA
<213> Streptococcus pneumoniae

<400> 141
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cccaaagcac cacgaatgaa ttggcgaagc aaggtttggt caaaccaacc tgtaaacatt 120
tccactaacc ataccaagag tgacaggccg ataaagaaa 159

<210> 142
<211> 144
<212> DNA
<213> Streptococcus pneumoniae

<400> 142
gattatttca agtttcgaac aacttttaca agattttcta cagtaaagcc atattctgcc 60
aatacttttg gtgctggggc agaggctccg aaggtatcaa tacctagaac ggcaccatcg 120
agaccaacat atttgtacca gttt 144

<210> 143
<211> 222
<212> DNA
<213> Streptococcus pneumoniae

<400> 143
agaggcagac gtggattatg cgttgcacga atcaaggctc ctagactagt cattaaacct 60
aagagaacaa tcgatccgcc taccaaagat agatacagtc caccactctc agctacatcc 120
ctctccgtcc ccaaaagtcc tatcatctct ttcccagcga agatggacaa aaatcctaaa 180
aggaaactta atagtaaggt aatcttcaac gcctcagtca ca 222

<210> 144

<211> 90

<212> DNA

<213> Streptococcus pneumoniae

<400> 144
actcctccat ataccaaaat tcctgccaaa acagctataa taccatttat ttcagctcaa 60

gatttcaacc aagcccaacg gctctctgga 90

<210> 145

<211> 122

<212> PRT

<213> Streptococcus pneumoniae

<400> 145

Met Ser Lys Asn Ile Val Gln Leu Asn Asn Ser Phe Ile Gln Asn Glu
1 5 10 15

Tyr Gln Arg Arg Arg Tyr Leu Met Lys Glu Arg Gln Lys Arg Asn Arg
20 25 30

Phe Met Gly Gly Val Leu Ile Leu Ile Met Leu Leu Phe Ile Leu Pro
35 40 45

Thr Phe Asn Leu Ala Gln Ser Tyr Gln Gln Leu Leu Gln Arg Arg Gln
50 55 60

Gln Leu Ala Asp Leu Gln Thr Gln Tyr Gln Thr Leu Ser Asp Glu Lys
65 70 75 80

Asp Lys Glu Thr Ala Phe Ala Thr Lys Leu Lys Asp Glu Asp Tyr Ala
85 90 95

Ala Lys Tyr Thr Arg Ala Lys Tyr Tyr Tyr Ser Lys Ser Arg Glu Lys
100 105 110

Val Tyr Thr Ile Pro Asp Leu Leu Gln Arg
115 120

<210> 146

<211> 877

<212> PRT

<213> Streptococcus pneumoniae

<400> 146

Met Asp Lys Lys Lys Leu Leu Leu Ile Asp Gly Ser Ser Val Ala Phe
1   5   10   15

Arg Ala Phe Phe Ala Leu Tyr Gln Gln Leu Asp Arg Phe Lys Asn Val
            20   25   30

Ala Gly Leu His Thr Asn Ala Ile Tyr Gly Phe Gln Leu Met Leu Ser
        35   40   45

His Leu Leu Glu Arg Val Glu Pro Ser His Ile Leu Val Ala Phe Asp
    50   55   60

Ala Gly Lys Thr Thr Phe Arg Thr Glu Met Tyr Ala Asp Tyr Lys Gly
65   70   75   80

Gly Arg Ala Lys Thr Pro Asp Glu Phe Arg Glu Gln Phe Pro Phe Ile
                85   90   95

Arg Glu Leu Leu Asp His Met Gly Ile Arg His Tyr Asp Leu Ala Gln
            100   105   110

Tyr Glu Ala Asp Asp Ile Ile Gly Thr Leu Asp Lys Leu Ala Glu Gln
        115   120   125

Asp Gly Phe Asp Ile Thr Ile Val Ser Gly Asp Lys Asp Leu Ile Gln
    130   135   140

Leu Thr Asp Glu His Thr Val Val Glu Ile Ser Lys Lys Gly Val Ala
145   150   155   160

Glu Phe Glu Ala Phe Thr Pro Asp Tyr Leu Met Glu Glu Met Gly Leu
                165   170   175

Thr Pro Ala Gln Phe Ile Asp Leu Lys Ala Leu Met Gly Asp Lys Ser
            180   185   190

Asp Asn Ile Pro Gly Val Thr Lys Val Gly Glu Lys Thr Gly Ile Lys
        195   200   205

Leu Leu Leu Glu His Gly Ser Leu Glu Gly Ile Tyr Glu Asn Ile Asp
    210   215   220

Gly Met Lys Thr Ser Lys Met Lys Glu Asn Leu Ile Asn Asp Lys Glu
225   230   235   240

Gln Ala Phe Leu Ser Lys Thr Leu Ala Thr Ile Asp Thr Lys Ala Pro
                245   250   255

Ile Ala Ile Gly Leu Glu Asp Leu Val Tyr Ser Gly Pro Asp Val Glu
260 265 270

Asn Leu Gly Lys Phe Tyr Asp Glu Met Gly Phe Lys Gln Leu Lys Gln
275 280 285

Ala Leu Asn Val Ser Ser Ala Asp Val Ser Glu Ser Leu Asp Phe Thr
290 295 300

Ile Val Asp Gln Ile Ser Gln Asp Met Leu Ser Glu Glu Ser Ile Phe
305 310 315 320

His Phe Glu Leu Phe Gly Glu Asn Tyr His Thr Asp Asn Leu Val Gly
325 330 335

Phe Val Trp Ser Cys Gly Asp Lys Leu Tyr Ala Thr Asp Lys Leu Glu
340 345 350

Leu Leu Gln Asp Pro Ile Phe Lys Asp Phe Leu Glu Lys Thr Ser Leu
355 360 365

Arg Val Tyr Asp Phe Lys Lys Val Lys Val Leu Leu Gln Arg Phe Gly
370 375 380

Val Asp Leu Gln Ala Pro Ala Phe Asp Ile Arg Leu Ala Lys Tyr Leu
385 390 395 400

Leu Ser Thr Val Glu Asp Asn Glu Ile Ala Thr Ile Ala Ser Leu Tyr
405 410 415

Gly Gln Thr Tyr Leu Val Asp Asp Glu Thr Phe Tyr Gly Lys Gly Val
420 425 430

Lys Lys Ala Ile Pro Glu Arg Glu Lys Phe Leu Glu His Leu Ala Cys
435 440 445

Lys Leu Ala Val Leu Val Glu Thr Glu Pro Ile Leu Leu Glu Lys Leu
450 455 460

Ser Glu Asn Gly Gln Leu Glu Leu Leu Tyr Asp Met Glu Gln Pro Leu
465 470 475 480

Ala Phe Val Leu Ala Lys Met Glu Ile Ala Gly Ile Met Val Lys Lys
485 490 495

Glu Thr Leu Leu Glu Met Gln Ala Glu Asn Glu Leu Val Ile Glu Lys
500 505 510

Leu Thr Gln Glu Ile Tyr Glu Leu Ala Gly Glu Glu Phe Asn Val Asn
515 520 525

Ser Pro Lys Gln Leu Gly Val Leu Leu Phe Glu Lys Leu Gly Leu Pro
530 535 540

Leu Glu Tyr Thr Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ala Val Asp
545 550 555 560

Val Leu Glu Arg Leu Ala Pro Ile Ala Pro Ile Val Lys Lys Ile Leu
565 570 575

Asp Tyr Arg Gln Ile Ala Lys Ile Gln Ser Thr Tyr Val Ile Gly Leu
580 585 590

Gln Asp Trp Ile Leu Ala Asp Gly Lys Ile His Thr Arg Tyr Val Gln
595 600 605

Asp Leu Thr Gln Thr Gly Arg Leu Ser Ser Val Asp Pro Asn Leu Gln
610 615 620

Asn Ile Pro Ala Arg Leu Glu Gln Gly Arg Leu Ile Arg Lys Ala Phe
625 630 635 640

Val Pro Glu Trp Glu Asp Ser Val Leu Leu Ser Ser Asp Tyr Ser Gln
645 650 655

Ile Glu Leu Arg Val Leu Ala His Ile Ser Lys Asp Glu His Leu Ile
660 665 670

Lys Ala Phe Gln Glu Gly Ala Asp Ile His Thr Ser Thr Ala Met Arg
675 680 685

Val Phe Gly Ile Glu Arg Pro Asp Asp Val Thr Ala Asn Asp Arg Arg
690 695 700

Asn Ala Lys Ala Val Asn Phe Gly Val Val Tyr Gly Ile Ser Asp Phe
705 710 715 720

Gly Leu Ser Asn Asn Leu Gly Ile Ser Arg Lys Glu Ala Lys Ala Tyr
725 730 735

Ile Asp Thr Tyr Phe Glu Arg Phe Pro Gly Ile Lys Asn Tyr Met Asp
740 745 750

Glu Val Val Arg Glu Ala Arg Asp Lys Gly Tyr Val Glu Thr Leu Phe
755 760 765

Lys Arg Arg Arg Glu Leu Pro Asp Ile Asn Ser Arg Asn Phe Asn Ile
770 775 780

Arg Gly Phe Ala Glu Arg Thr Ala Ile Asn Ser Pro Ile Gln Gly Ser
785 790 795 800

Ala Ala Asp Ile Leu Lys Ile Ala Met Ile Gln Leu Asp Lys Ala Leu
805 810 815

Val Ala Gly Gly Tyr Gln Thr Lys Met Leu Leu Gln Val His Asp Glu
820 825 830

Ile Val Leu Glu Val Pro Lys Ser Glu Leu Val Glu Met Lys Lys Leu
835 840 845

Val Lys Gln Thr Met Glu Glu Ala Ile Gln Leu Ser Val Pro Leu Ile
850 855 860

Ala Asp Glu Asn Glu Gly Ala Thr Trp Tyr Glu Ala Lys
865 870 875

<210> 147

<211> 211

<212> PRT

<213> Streptococcus pneumoniae

<400> 147

Met Gly Met Ala Ala Phe Lys Asn Pro Asn Asn Gln Tyr Lys Ala Ile
1 5 10 15

Thr Ile Ala Gln Thr Leu Gly Asp Asp Ala Ser Ser Glu Glu Leu Ala
20 25 30

Gly Arg Tyr Gly Ser Ala Val Gln Cys Thr Glu Val Thr Ala Ser Asn
35 40 45

Leu Ser Thr Val Lys Thr Lys Ala Thr Val Val Glu Lys Pro Leu Lys
50 55 60

Asp Phe Arg Ala Ser Thr Ser Asp Gln Ser Gly Trp Val Glu Ser Asn
65 70 75 80

Gly Lys Trp Tyr Phe Tyr Glu Ser Gly Asp Val Lys Thr Gly Trp Val
85 90 95

Lys Thr Asp Gly Lys Trp Tyr Tyr Leu Asn Asp Leu Gly Val Met Gln
100 105 110

Thr Gly Phe Val Lys Phe Ser Gly Ser Trp Tyr Tyr Leu Ser Asn Ser
115 120 125

Gly Ala Met Phe Thr Gly Trp Gly Thr Asp Gly Ser Arg Trp Phe Tyr
130 135 140

Phe Asp Gly Ser Gly Ala Met Lys Thr Gly Trp Tyr Lys Glu Asn Gly
145 150 155 160

Thr Trp Tyr Tyr Leu Asp Glu Ala Gly Ile Met Lys Thr Gly Trp Phe
165 170 175

Lys Val Gly Pro His Trp Tyr Tyr Ala Tyr Gly Ser Gly Ala Leu Ala
180 185 190

Val Ser Thr Thr Thr Pro Asp Gly Tyr Arg Val Asn Gly Asn Gly Glu
195 200 205

Trp Val Asn
210

<210> 148

<211> 1856

<212> PRT

<213> Streptococcus pneumoniae

<400> 148

Met Ser Arg Lys Ser Ile Gly Glu Lys Arg His Ser Phe Ser Met Arg
1 5 10 15

Lys Leu Ser Val Gly Leu Val Ser Val Thr Val Ser Ser Phe Phe Leu
20 25 30

Met Ser Gln Gly Ile Gln Ser Val Ser Ala Asp Asn Met Glu Ser Pro
35 40 45

Ile His Tyr Lys Tyr Met Thr Glu Gly Lys Leu Thr Asp Glu Glu Lys
50 55 60

Ser Leu Leu Val Glu Ala Leu Pro Gln Leu Ala Glu Glu Ser Asp Asp
65 70 75 80

Thr Tyr Tyr Leu Val Tyr Arg Ser Gln Gln Phe Leu Pro Asn Thr Gly
85 90 95

Phe Asn Pro Thr Val Gly Thr Phe Leu Phe Thr Ala Gly Leu Ser Leu
100 105 110

Leu Val Leu Leu Val Ser Lys Arg Glu Asn Gly Lys Lys Arg Leu Val
115 120 125

His Phe Leu Leu Leu Thr Ser Met Gly Val Gln Leu Leu Pro Ala Ser
130 135 140

```
Ala Phe Gly Leu Thr Ser Gln Ile Leu Ser Ala Tyr Asn Ser Gln Leu
145                 150                 155                 160

Ser Ile Gly Val Gly Glu His Leu Pro Glu Pro Leu Lys Ile Glu Gly
                165                 170                 175

Tyr Gln Tyr Ile Gly Tyr Ile Lys Thr Lys Lys Gln Asp Asn Thr Glu
            180                 185                 190

Leu Ser Arg Thr Val Asp Gly Lys Tyr Ser Ala Gln Arg Asp Ser Gln
        195                 200                 205

Pro Asn Ser Thr Lys Thr Ser Asp Val Val His Ser Ala Asp Leu Glu
    210                 215                 220

Trp Asn Gln Gly Gln Gly Lys Val Ser Leu Gln Gly Glu Ala Ser Gly
225                 230                 235                 240

Asp Asp Gly Leu Ser Glu Lys Ser Ser Ile Ala Ala Asp Asn Leu Ser
                245                 250                 255

Ser Asn Asp Ser Phe Ala Ser Gln Val Glu Gln Asn Pro Asp His Lys
            260                 265                 270

Gly Glu Ser Val Val Arg Pro Thr Val Pro Glu Gln Gly Asn Pro Val
        275                 280                 285

Ser Ala Thr Thr Val Gln Ser Ala Glu Glu Glu Val Leu Ala Thr Thr
    290                 295                 300

Asn Asp Arg Pro Glu Tyr Lys Leu Pro Leu Glu Thr Lys Gly Thr Gln
305                 310                 315                 320

Glu Pro Gly His Glu Gly Glu Ala Ala Val Arg Glu Asp Leu Pro Val
                325                 330                 335

Tyr Thr Lys Pro Leu Glu Thr Lys Gly Thr Gln Gly Pro Gly His Glu
            340                 345                 350

Gly Glu Ala Ala Val Arg Glu Glu Glu Pro Ala Tyr Thr Glu Pro Leu
        355                 360                 365

Ala Thr Lys Gly Thr Gln Glu Pro Gly His Glu Gly Lys Ala Thr Val
    370                 375                 380

Arg Glu Glu Thr Leu Glu Tyr Thr Glu Pro Val Ala Thr Lys Gly Thr
385                 390                 395                 400

Gln Glu Pro Glu His Glu Gly Glu Ala Ala Val Glu Glu Glu Leu Pro
                405                 410                 415
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Ala Leu Glu Val Thr Thr Arg Asn Arg Thr Glu Ile Gln Asn Ile Pro
420 425 430

Tyr Thr Thr Glu Glu Ile Gln Asp Pro Thr Leu Leu Lys Asn Arg Arg
435 440 445

Lys Ile Glu Arg Gln Gly Gln Ala Gly Thr Arg Thr Ile Gln Tyr Glu
450 455 460

Asp Tyr Ile Val Asn Gly Asn Val Val Glu Thr Lys Glu Val Ser Arg
465 470 475 480

Thr Glu Val Ala Pro Val Asn Glu Val Val Lys Val Gly Thr Leu Val
485 490 495

Lys Val Lys Pro Thr Val Glu Ile Thr Asn Leu Thr Lys Val Glu Asn
500 505 510

Lys Lys Ser Ile Thr Val Ser Tyr Asn Leu Ile Asp Thr Thr Ser Ala
515 520 525

Tyr Val Ser Ala Lys Thr Gln Val Phe His Gly Asp Lys Leu Val Lys
530 535 540

Glu Val Asp Ile Glu Asn Pro Ala Lys Glu Gln Val Ile Ser Gly Leu
545 550 555 560

Asp Tyr Tyr Thr Pro Tyr Thr Val Lys Thr His Leu Thr Tyr Asn Leu
565 570 575

Gly Glu Asn Asn Glu Glu Asn Thr Glu Thr Ser Thr Gln Asp Phe Gln
580 585 590

Leu Glu Tyr Lys Lys Ile Glu Ile Lys Asp Ile Asp Ser Val Glu Leu
595 600 605

Tyr Gly Lys Glu Asn Asp Arg Tyr Arg Arg Tyr Leu Ser Leu Ser Glu
610 615 620

Ala Pro Thr Asp Thr Ala Lys Tyr Phe Val Lys Val Lys Ser Asp Arg
625 630 635 640

Phe Lys Glu Met Tyr Leu Pro Val Lys Ser Ile Thr Glu Asn Thr Asp
645 650 655

Gly Thr Tyr Lys Val Thr Val Ala Val Asp Gln Leu Val Glu Glu Gly
660 665 670

Thr Asp Gly Tyr Lys Asp Asp Tyr Thr Phe Thr Val Ala Lys Ser Lys
675 680 685

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Ala Glu Gln Pro Gly Val Tyr Thr Ser Phe Lys Gln Leu Val Thr Ala
    690                 695                 700

Met Gln Ser Asn Leu Ser Gly Val Tyr Thr Leu Ala Ser Asp Met Thr
705                 710                 715                 720

Ala Asp Glu Val Ser Leu Gly Asp Lys Gln Thr Ser Tyr Leu Thr Gly
                725                 730                 735

Ala Phe Thr Gly Ser Leu Ile Gly Ser Asp Gly Thr Lys Ser Tyr Ala
            740                 745                 750

Ile Tyr Asp Leu Lys Lys Pro Leu Phe Asp Thr Leu Asn Gly Ala Thr
        755                 760                 765

Val Arg Asp Leu Asp Ile Lys Thr Val Ser Ala Asp Ser Lys Glu Asn
    770                 775                 780

Val Ala Ala Leu Ala Lys Ala Ala Asn Ser Ala Asn Ile Asn Asn Val
785                 790                 795                 800

Ala Val Glu Gly Lys Ile Ser Gly Ala Lys Ser Val Ala Gly Leu Val
                805                 810                 815

Ala Ser Ala Thr Asn Thr Val Ile Glu Asn Ser Ser Phe Thr Gly Lys
            820                 825                 830

Leu Ile Ala Asn His Gln Asp Ser Asn Lys Asn Asp Thr Gly Gly Ile
        835                 840                 845

Val Gly Asn Ile Thr Gly Asn Ser Ser Arg Val Asn Lys Val Arg Val
    850                 855                 860

Asp Ala Leu Ile Ser Thr Asn Ala Arg Asn Asn Asn Gln Thr Ala Gly
865                 870                 875                 880

Gly Ile Val Gly Arg Leu Glu Asn Gly Ala Leu Ile Ser Asn Ser Val
                885                 890                 895

Ala Thr Gly Glu Ile Arg Asn Gly Gln Gly Tyr Ser Arg Val Gly Gly
            900                 905                 910

Ile Val Gly Ser Thr Trp Gln Asn Gly Arg Val Asn Asn Val Val Ser
        915                 920                 925

Asn Val Asp Val Gly Asp Gly Tyr Val Ile Thr Gly Asp Gln Tyr Ala
    930                 935                 940

Ala Ala Asp Val Lys Asn Ala Ser Thr Ser Val Asp Asn Arg Lys Ala
945                 950                 955                 960
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Asp Arg Phe Ala Thr Lys Leu Ser Lys Asp Gln Ile Asp Ala Lys Val
965 970 975

Ala Asp Tyr Gly Ile Thr Val Thr Leu Asp Asp Thr Gly Gln Asp Leu
980 985 990

Lys Arg Asn Leu Arg Glu Val Asp Tyr Thr Arg Leu Asn Lys Ala Glu
995 1000 1005

Ala Glu Arg Lys Val Ala Tyr Ser Asn Ile Glu Lys Leu Met Pro
1010 1015 1020

Phe Tyr Asn Lys Asp Leu Val Val His Tyr Gly Asn Lys Val Ala
1025 1030 1035

Thr Thr Asp Lys Leu Tyr Thr Thr Glu Leu Leu Asp Val Val Pro
1040 1045 1050

Met Lys Asp Asp Glu Val Val Thr Asp Ile Asn Asn Lys Lys Asn
1055 1060 1065

Ser Ile Asn Lys Val Met Leu His Phe Lys Asp Asn Thr Val Glu
1070 1075 1080

Tyr Leu Asp Val Thr Phe Lys Glu Asn Phe Ile Asn Ser Gln Val
1085 1090 1095

Ile Glu Tyr Asn Val Thr Gly Lys Glu Tyr Ile Phe Thr Pro Glu
1100 1105 1110

Ala Phe Val Ser Asp Tyr Thr Ala Ile Thr Asn Asn Val Leu Ser
1115 1120 1125

Asp Leu Gln Asn Val Thr Leu Asn Ser Glu Ala Thr Lys Lys Val
1130 1135 1140

Leu Gly Ala Ala Asn Asp Ala Ala Leu Asp Asn Leu Tyr Leu Asp
1145 1150 1155

Arg Gln Phe Glu Glu Val Lys Ala Asn Ile Ala Glu His Leu Arg
1160 1165 1170

Lys Val Leu Ala Met Asp Lys Ser Ile Asn Thr Thr Gly Asp Gly
1175 1180 1185

Val Val Glu Tyr Val Ser Glu Lys Ile Lys Asn Asn Lys Glu Ala
1190 1195 1200

Phe Met Leu Gly Leu Thr Tyr Met Asn Arg Trp Tyr Asp Ile Asn
1205 1210 1215

Tyr Gly Lys Met Asn Thr Lys Asp Leu Ser Thr Tyr Lys Phe Asp
1220 1225 1230

Phe Asn Gly Asn Asn Glu Thr Ser Thr Leu Asp Thr Ile Val Ala
1235 1240 1245

Leu Gly Asn Ser Gly Leu Asp Asn Leu Arg Ala Ser Asn Thr Val
1250 1255 1260

Gly Leu Tyr Ala Asn Lys Leu Ala Ser Val Lys Gly Glu Asp Ser
1265 1270 1275

Val Phe Asp Phe Val Glu Ala Tyr Arg Lys Leu Phe Leu Pro Asn
1280 1285 1290

Lys Thr Asn Asn Glu Trp Phe Lys Glu Asn Thr Lys Ala Tyr Ile
1295 1300 1305

Val Glu Met Lys Ser Asp Ile Ala Glu Val Arg Glu Lys Gln Glu
1310 1315 1320

Ser Pro Thr Ala Asp Arg Lys Tyr Ser Leu Gly Val Tyr Asp Arg
1325 1330 1335

Ile Ser Ala Pro Ser Trp Gly His Lys Ser Met Leu Leu Pro Leu
1340 1345 1350

Leu Thr Leu Pro Glu Glu Ser Val Tyr Ile Ser Ser Asn Met Ser
1355 1360 1365

Thr Leu Ala Phe Gly Ser Tyr Glu Arg Tyr Arg Asp Ser Val Asp
1370 1375 1380

Gly Val Ile Leu Ser Gly Asp Ala Leu Arg Thr Tyr Val Arg Asn
1385 1390 1395

Arg Val Asp Ile Ala Ala Lys Arg His Arg Asp His Tyr Asp Ile
1400 1405 1410

Trp Tyr Asn Leu Leu Asp Ser Ala Ser Lys Glu Lys Leu Phe Arg
1415 1420 1425

Ser Val Ile Val Tyr Asp Gly Phe Asn Val Lys Asp Glu Thr Gly
1430 1435 1440

Arg Thr Tyr Trp Ala Arg Leu Thr Asp Lys Asn Ile Gly Ser Ile
1445 1450 1455

Lys Glu Phe Phe Gly Pro Val Gly Lys Trp Tyr Glu Tyr Asn Ser
1460 1465 1470

Ser Ala Gly Ala Tyr Ala Asn Gly Ser Leu Thr His Phe Val Leu
1475 1480 1485

Asp Arg Leu Leu Asp Ala Tyr Gly Thr Ser Val Tyr Thr His Glu
1490 1495 1500

Met Val His Asn Ser Asp Ser Ala Ile Tyr Phe Glu Gly Asn Gly
1505 1510 1515

Arg Arg Glu Gly Leu Gly Ala Glu Leu Tyr Ala Leu Gly Leu Leu
1520 1525 1530

Gln Ser Val Asp Ser Val Asn Ser His Ile Leu Ala Leu Asn Thr
1535 1540 1545

Leu Tyr Lys Ala Glu Lys Asp Asp Leu Asn Arg Leu His Thr Tyr
1550 1555 1560

Asn Pro Val Glu Arg Phe Asp Ser Asp Glu Ala Leu Gln Ser Tyr
1565 1570 1575

Met His Gly Ser Tyr Asp Val Met Tyr Thr Leu Asp Ala Met Glu
1580 1585 1590

Ala Lys Ala Ile Leu Ala Gln Asn Asn Asp Val Lys Lys Lys Trp
1595 1600 1605

Phe Arg Lys Ile Glu Asn Tyr Tyr Val Arg Asp Thr Arg His Asn
1610 1615 1620

Lys Asp Thr His Ala Gly Asn Lys Val Arg Pro Leu Thr Asp Glu
1625 1630 1635

Glu Val Ala Asn Leu Thr Ser Leu Asn Ser Leu Ile Asp Asn Asp
1640 1645 1650

Ile Ile Asn Arg Arg Ser Tyr Asp Asp Ser Arg Glu Tyr Lys Arg
1655 1660 1665

Asn Gly Tyr Tyr Thr Ile Ser Met Phe Ser Pro Val Tyr Ala Ala
1670 1675 1680

Leu Ser Asn Ser Lys Gly Ala Pro Gly Asp Ile Met Phe Arg Lys
1685 1690 1695

Ile Ala Tyr Glu Leu Leu Ala Glu Lys Gly Tyr His Lys Gly Phe
1700 1705 1710

Leu Pro Tyr Val Ser Asn Gln Tyr Gly Ala Glu Ala Phe Ala Ser
1715 1720 1725

Gly Ser Lys Thr Phe Ser Ser Trp His Gly Arg Asp Val Ala Leu
1730 1735 1740

Val Thr Asp Asp Leu Val Phe Lys Lys Val Phe Asn Gly Glu Tyr
1745 1750 1755

Ser Ser Trp Ala Asp Phe Lys Lys Ala Met Phe Lys Gln Arg Ile
1760 1765 1770

Asp Lys Gln Asp Asn Leu Lys Pro Ile Thr Ile Gln Tyr Glu Leu
1775 1780 1785

Gly Asn Pro Asn Ser Thr Lys Glu Val Thr Ile Thr Thr Ala Ala
1790 1795 1800

Gln Met Gln Gln Leu Ile Asn Glu Ala Ala Ala Lys Asp Ile Thr
1805 1810 1815

Asn Ile Asp Arg Ala Thr Ser His Thr Pro Ala Ser Trp Val His
1820 1825 1830

Leu Leu Lys Gln Lys Ile Tyr Asn Ala Tyr Leu Arg Thr Thr Asp
1835 1840 1845

Asp Phe Arg Asn Ser Ile Tyr Lys
1850 1855

<210> 149

<211> 857

<212> PRT

<213> Streptococcus pneumoniae

<400> 149

Met Lys Phe Asn Pro Asn Gln Arg Tyr Thr Arg Trp Ser Ile Arg Arg
1 5 10 15

Leu Ser Val Gly Val Ala Ser Val Val Val Ala Ser Gly Phe Phe Val
20 25 30

Leu Val Gly Gln Pro Ser Ser Val Arg Ala Asp Gly Leu Asn Pro Thr
35 40 45

Pro Gly Gln Val Leu Pro Glu Glu Thr Ser Gly Thr Lys Glu Gly Asp
50 55 60

Leu Ser Glu Lys Pro Gly Asp Thr Val Leu Thr Gln Ala Lys Pro Glu
65 70 75 80

Gly Val Thr Gly Asn Thr Asn Ser Leu Pro Thr Pro Thr Glu Arg Thr
85 90 95

Glu Val Ser Glu Glu Thr Ser Pro Ser Ser Leu Asp Thr Leu Phe Glu
100 105 110

Lys Asp Glu Glu Ala Gln Lys Asn Pro Glu Leu Thr Asp Val Leu Lys
115 120 125

Glu Thr Val Asp Thr Ala Asp Val Asp Gly Thr Gln Ala Ser Pro Ala
130 135 140

Glu Thr Thr Pro Glu Gln Val Lys Gly Gly Val Lys Glu Asn Thr Lys
145 150 155 160

Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu Glu Lys Ala Glu Gly Lys
165 170 175

Gly Pro Phe Thr Ala Gly Val Asn Gln Val Ile Pro Tyr Glu Leu Phe
180 185 190

Ala Gly Asp Gly Met Leu Thr Arg Leu Leu Leu Lys Ala Ser Asp Asn
195 200 205

Ala Pro Trp Ser Asp Asn Gly Thr Ala Lys Asn Pro Ala Leu Pro Pro
210 215 220

Leu Glu Gly Leu Thr Lys Gly Lys Tyr Phe Tyr Glu Val Asp Leu Asn
225 230 235 240

Gly Asn Thr Val Gly Lys Gln Gly Gln Ala Leu Ile Asp Gln Leu Arg
245 250 255

Ala Asn Gly Thr Gln Thr Tyr Lys Ala Thr Val Lys Val Tyr Gly Asn
260 265 270

Lys Asp Gly Lys Ala Asp Leu Thr Asn Leu Val Ala Thr Lys Asn Val
275 280 285

Asp Ile Asn Ile Asn Gly Leu Val Ala Lys Glu Thr Val Gln Lys Ala
290 295 300

Val Ala Asp Asn Val Lys Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu
305 310 315 320

Glu Lys Ala Lys Gly Glu Gly Pro Phe Thr Ala Gly Val Asn His Val
325 330 335

Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu
340 345 350

Leu Lys Ala Ser Asp Lys Ala Pro Trp Ser Asp Asn Gly Asp Ala Lys
355 360 365

Asn Pro Ala Leu Ser Pro Leu Gly Glu Asn Val Lys Thr Lys Gly Gln
370 375 380

Tyr Phe Tyr Gln Val Ala Leu Asp Gly Asn Val Ala Gly Lys Glu Lys
385 390 395 400

Gln Ala Leu Ile Asp Gln Phe Arg Ala Asn Gly Thr Gln Thr Tyr Ser
405 410 415

Ala Thr Val Asn Val Tyr Gly Asn Lys Asp Gly Lys Pro Asp Leu Asp
420 425 430

Asn Ile Val Ala Thr Lys Lys Val Thr Ile Asn Ile Asn Gly Leu Ile
435 440 445

Ser Lys Glu Thr Val Gln Lys Ala Val Ala Asp Asn Val Lys Asp Ser
450 455 460

Ile Asp Val Pro Ala Ala Tyr Leu Glu Lys Ala Lys Gly Glu Gly Pro
465 470 475 480

Phe Thr Ala Gly Val Asn His Val Ile Pro Tyr Glu Leu Phe Ala Gly
485 490 495

Asp Gly Met Leu Thr Arg Leu Leu Leu Lys Ala Ser Asp Lys Ala Pro
500 505 510

Trp Ser Asp Asn Gly Asp Ala Lys Asn Pro Ala Leu Ser Pro Leu Gly
515 520 525

Glu Asn Val Lys Thr Lys Gly Gln Tyr Phe Tyr Gln Leu Ala Leu Asp
530 535 540

Gly Asn Val Ala Gly Lys Glu Lys Gln Ala Leu Ile Asp Gln Phe Arg
545 550 555 560

Ala Asn Gly Thr Gln Thr Tyr Ser Ala Thr Val Asn Val Tyr Gly Asn
565 570 575

Lys Asp Gly Lys Pro Asp Leu Asp Asn Ile Val Ala Thr Lys Lys Val
580 585 590

Thr Ile Asn Ile Asn Gly Leu Ile Ser Lys Glu Thr Val Gln Lys Ala
595 600 605

Val Ala Asp Asn Val Lys Asp Ser Ile Asp Val Pro Ala Ala Tyr Leu
610 615 620

Glu Lys Ala Lys Gly Glu Gly Pro Phe Thr Ala Gly Val Asn His Val
625 630 635 640

Ile Pro Tyr Glu Leu Phe Ala Gly Asp Gly Met Leu Thr Arg Leu Leu
645 650 655

Leu Lys Ala Ser Asp Lys Ala Pro Trp Ser Asp Asn Gly Asp Ala Lys
660 665 670

Asn Pro Ala Leu Ser Pro Leu Gly Glu Asn Val Lys Thr Lys Gly Gln
675 680 685

Tyr Phe Tyr Gln Val Ala Leu Asp Gly Asn Val Ala Gly Lys Glu Lys
690 695 700

Gln Ala Leu Ile Asp Gln Phe Arg Ala Asn Gly Thr Gln Thr Tyr Ser
705 710 715 720

Ala Thr Val Asn Val Tyr Gly Asn Lys Asp Gly Lys Pro Asp Leu Asp
725 730 735

Asn Ile Val Ala Thr Lys Lys Val Thr Ile Lys Ile Asn Val Lys Glu
740 745 750

Thr Ser Asp Thr Ala Asn Gly Ser Leu Ser Pro Ser Asn Ser Gly Ser
755 760 765

Gly Val Thr Pro Met Asn His Asn His Ala Thr Gly Thr Thr Asp Ser
770 775 780

Met Pro Ala Asp Thr Met Thr Ser Ser Thr Asn Thr Met Ala Gly Glu
785 790 795 800

Asn Met Ala Ala Ser Ala Asn Lys Met Ser Asp Thr Met Met Ser Glu
805 810 815

Asp Lys Ala Met Leu Pro Asn Thr Gly Glu Thr Gln Thr Ser Met Ala
820 825 830

Ser Ile Gly Phe Leu Gly Leu Ala Leu Ala Gly Leu Leu Gly Gly Leu
835 840 845

Gly Leu Lys Asn Lys Lys Glu Glu Asn
850 855

<210> 150

<211> 195

<212> PRT

<213> Streptococcus pneumoniae

<400> 150

Met Lys Ser Ile Thr Lys Lys Ile Lys Ala Thr Leu Ala Gly Val Ala
1 5 10 15

Ala Leu Phe Ala Val Phe Ala Pro Ser Phe Val Ser Ala Gln Glu Ser
20 25 30

Ser Thr Tyr Thr Val Lys Glu Gly Asp Thr Leu Ser Glu Ile Ala Glu
35 40 45

Thr His Asn Thr Thr Val Glu Lys Leu Ala Glu Asn Asn His Ile Asp
50 55 60

Asn Ile His Leu Ile Tyr Val Asp Gln Glu Leu Val Ile Asp Gly Pro
65 70 75 80

Val Ala Pro Val Ala Thr Pro Ala Pro Ala Thr Tyr Ala Ala Pro Ala
85 90 95

Ala Gln Asp Glu Thr Val Ser Ala Pro Val Ala Glu Thr Pro Val Val
100 105 110

Ser Glu Thr Val Val Ser Thr Val Ser Gly Ser Glu Ala Glu Ala Lys
115 120 125

Glu Trp Ile Ala Gln Lys Glu Ser Gly Gly Ser Tyr Thr Ala Thr Asn
130 135 140

Gly Arg Tyr Ile Gly Arg Tyr Gln Leu Thr Asp Ser Tyr Leu Asn Gly
145 150 155 160

Asp Tyr Ser Ala Glu Asn Gln Glu Arg Val Ala Asp Ala Tyr Val Ala
165 170 175

Gly Arg Tyr Gly Ser Trp Thr Ala Ala Lys Asn Phe Trp Leu Asn Asn
180 185 190

Gly Trp Tyr
195

<210> 151

<211> 744

<212> PRT

<213> Streptococcus pneumoniae

<400> 151

Met Asn Lys Lys Lys Met Ile Leu Thr Ser Leu Ala Ser Val Ala Ile
1   5   10   15

Leu Gly Ala Gly Phe Val Thr Ser Gln Pro Thr Phe Val Arg Ala Glu
            20   25   30

Glu Ser Pro Gln Val Val Glu Lys Ser Ser Leu Glu Lys Lys Tyr Glu
        35   40   45

Glu Ala Lys Ala Lys Ala Asp Thr Ala Lys Lys Asp Tyr Glu Thr Ala
    50   55   60

Lys Lys Lys Ala Glu Asp Ala Gln Lys Lys Tyr Glu Asp Asp Gln Lys
65   70   75   80

Arg Thr Glu Glu Lys Ala Arg Lys Glu Ala Glu Ala Ser Gln Lys Leu
                85   90   95

Asn Asp Val Ala Leu Val Val Gln Asn Ala Tyr Lys Glu Tyr Arg Glu
            100   105   110

Val Gln Asn Gln Arg Ser Lys Tyr Lys Ser Asp Ala Glu Tyr Gln Lys
        115   120   125

Lys Leu Thr Glu Val Asp Ser Lys Ile Glu Lys Ala Arg Lys Glu Gln
    130   135   140

Gln Asp Leu Gln Asn Lys Phe Asn Glu Val Arg Ala Val Val Val Pro
145   150   155   160

Glu Pro Asn Ala Leu Ala Glu Thr Lys Lys Lys Ala Glu Glu Ala Lys
                165   170   175

Ala Glu Glu Lys Val Ala Lys Arg Lys Tyr Asp Tyr Ala Thr Leu Lys
            180   185   190

Val Ala Leu Ala Lys Lys Glu Val Glu Ala Lys Glu Leu Glu Ile Glu
        195   200   205

Lys Leu Gln Tyr Glu Ile Ser Thr Leu Glu Gln Glu Val Ala Thr Ala
    210   215   220

Gln His Gln Val Asp Asn Leu Lys Lys Leu Leu Ala Gly Ala Asp Pro
225   230   235   240

Asp Asp Gly Thr Glu Val Ile Glu Ala Lys Leu Lys Lys Gly Glu Ala
                245   250   255

Glu Leu Asn Ala Lys Gln Ala Glu Leu Ala Lys Lys Gln Thr Glu Leu
            260   265   270

Glu Lys Leu Leu Asp Ser Leu Asp Pro Glu Gly Lys Thr Gln Asp Glu
275 280 285

Leu Asp Lys Glu Ala Glu Glu Ala Glu Leu Asp Lys Lys Ala Asp Glu
290 295 300

Leu Gln Asn Lys Val Ala Asp Leu Glu Lys Glu Ile Ser Asn Leu Glu
305 310 315 320

Ile Leu Leu Gly Gly Ala Asp Pro Glu Asp Asp Thr Ala Ala Leu Gln
325 330 335

Asn Lys Leu Ala Ala Lys Lys Ala Glu Leu Ala Lys Lys Gln Thr Glu
340 345 350

Leu Glu Lys Leu Leu Asp Ser Leu Asp Pro Glu Gly Lys Thr Gln Asp
355 360 365

Glu Leu Asp Lys Glu Ala Glu Glu Ala Glu Leu Asp Lys Lys Ala Asp
370 375 380

Glu Leu Gln Asn Lys Val Ala Asp Leu Glu Lys Glu Ile Ser Asn Leu
385 390 395 400

Glu Ile Leu Leu Gly Gly Ala Asp Ser Glu Asp Asp Thr Ala Ala Leu
405 410 415

Gln Asn Lys Leu Ala Thr Lys Lys Ala Glu Leu Glu Lys Thr Gln Lys
420 425 430

Glu Leu Asp Ala Ala Leu Asn Glu Leu Gly Pro Asp Gly Asp Glu Glu
435 440 445

Glu Thr Pro Ala Pro Ala Pro Gln Pro Glu Gln Pro Ala Pro Ala Pro
450 455 460

Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Pro
465 470 475 480

Ala Pro Lys Pro Glu Gln Pro Ala Pro Ala Pro Lys Pro Glu Gln Pro
485 490 495

Ala Pro Ala Pro Lys Pro Glu Gln Pro Ala Lys Pro Glu Lys Pro Ala
500 505 510

Glu Glu Pro Thr Gln Pro Glu Lys Pro Ala Thr Pro Lys Thr Gly Trp
515 520 525

Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr Asp Gly Ser Met
530 535 540

Ala Ile Gly Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ala
545 550 555 560

Asn Gly Ala Met Ala Thr Gly Trp Val Lys Asp Gly Asp Thr Trp Tyr
565 570 575

Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser Gln Trp Phe Lys Val
580 585 590

Ser Asp Lys Trp Tyr Tyr Val Asn Ser Asn Gly Ala Met Ala Thr Gly
595 600 605

Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Asp
610 615 620

Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn
625 630 635 640

Ala Asn Gly Asp Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp
645 650 655

Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val
660 665 670

Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser Met Ala Thr Gly
675 680 685

Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala
690 695 700

Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val
705 710 715 720

Asn Gly Leu Gly Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Lys
725 730 735

Val Asn Ala Asn Gly Glu Trp Val
740

<210> 152

<211> 189

<212> PRT

<213> Streptococcus pneumoniae

<400> 152

Met Lys Lys Ile Val Leu Val Ser Leu Ala Phe Leu Phe Val Leu Val
1 5 10 15

Gly Cys Gly Gln Lys Lys Glu Thr Gly Pro Ala Thr Lys Thr Glu Lys
20 25 30

Asp Thr Leu Gln Ser Ala Leu Pro Val Ile Glu Asn Ala Glu Lys Asn
35 40 45

Thr Val Val Thr Lys Thr Leu Val Leu Pro Lys Ser Asp Asp Gly Ser
50 55 60

Gln Gln Thr Gln Thr Ile Thr Tyr Lys Asp Lys Thr Phe Leu Ser Leu
65 70 75 80

Ala Ile Gln Gln Lys Arg Pro Val Ser Asp Glu Leu Lys Thr Tyr Ile
85 90 95

Asp Gln His Gly Val Glu Glu Thr Gln Lys Ala Leu Leu Glu Ala Glu
100 105 110

Glu Lys Asp Lys Ser Ile Ile Glu Ala Arg Lys Leu Ala Gly Phe Lys
115 120 125

Leu Glu Thr Lys Leu Leu Ser Ala Thr Glu Leu Gln Thr Thr Thr Ser
130 135 140

Phe Asp Phe Gln Val Leu Asp Val Lys Lys Ala Ser Gln Leu Glu His
145 150 155 160

Leu Lys Asn Ile Gly Leu Glu Asn Leu Leu Lys Asn Glu Pro Ser Lys
165 170 175

Tyr Ile Ser Asp Arg Leu Ala Asn Gly Ala Thr Glu Gln
180 185

<210> 153

<211> 416

<212> PRT

<213> Streptococcus pneumoniae

<400> 153

Met Phe Glu Val Glu Glu Trp Leu His Ser Arg Ile Gly Leu Asn Phe
1 5 10 15

Arg Ser Gly Leu Gly Arg Met Gln Gln Ala Val Asp Leu Leu Gly Asn
20 25 30

Pro Glu Gln Ser Tyr Pro Ile Ile His Val Thr Gly Thr Asn Gly Lys
35 40 45

Gly Ser Thr Ile Ala Phe Met Arg Glu Leu Phe Met Gly His Gly Lys
50 55 60

Lys Val Ala Thr Phe Thr Ser Pro His Ile Val Ser Ile Asn Asp Arg
65 70 75 80

Ile Cys Ile Asn Gly Gln Pro Ile Ala Asp Ala Asp Phe Ile Arg Leu
85 90 95

Thr Asp Gln Val Lys Glu Met Glu Lys Thr Leu Leu Gln Thr Pro Ala
100 105 110

Gln Leu Ser Phe Phe Glu Leu Leu Thr Leu Val Ala Phe Leu Tyr Phe
115 120 125

Arg Glu Gln Glu Val Asp Leu Val Leu Leu Glu Val Gly Ile Gly Gly
130 135 140

Leu Leu Asp Thr Thr Asn Val Val Thr Gly Glu Phe Ala Val Ile Thr
145 150 155 160

Ser Ile Gly Leu Asp His Gln Glu Thr Leu Gly Asp Ser Leu Glu Ala
165 170 175

Ile Ala Glu Gln Lys Ala Gly Ile Phe Lys Ala Gly Lys Lys Ala Val
180 185 190

Ile Ala Lys Leu Pro Pro Glu Ala Arg Leu Ala Cys Gln Lys Lys Ala
195 200 205

Glu Ser Leu Ala Val Asn Leu Tyr Gln Ala Gly Gln Asp Phe Leu Met
210 215 220

Leu Asn Gly Asp Phe Ser Ser Ser Leu Leu Asn Leu Ser Gln Leu Asn
225 230 235 240

Ile Gly Leu Glu Gly Val Tyr Gln Gln Glu Asn Ala Ala Leu Ala Leu
245 250 255

Gln Thr Phe Leu Leu Phe Met Arg Glu Arg Lys Glu Ala Val Asp Glu
260 265 270

Gln Ala Val Arg Lys Ala Leu Glu Gln Thr His Trp Ala Gly Arg Leu
275 280 285

Glu Arg Ile Arg Pro Gln Ile Tyr Leu Asp Gly Ala His Asn Leu Pro
290 295 300

Ala Leu Thr Arg Leu Ala Glu Phe Ile Lys Glu Lys Glu Gln Glu Gly
305 310 315 320

Tyr Arg Pro Gln Ile Leu Phe Gly Ser Leu Lys Arg Lys Asp Tyr Gln
325 330 335

Gly Met Leu Gly Tyr Leu Thr Glu Lys Leu Pro Gln Val Glu Leu Lys
340 345 350

Val Thr Gly Phe Asp Tyr Gln Gly Ala Leu Asp Glu Arg Asp Val Thr
355 360 365

Gly Tyr Asp Ile Val Ser Ser Tyr Arg Glu Phe Ile Ser Asp Phe Glu
370 375 380

Glu Arg Ala Asp Ala Gln Asp Leu Leu Phe Val Thr Gly Ser Leu Tyr
385 390 395 400

Phe Ile Ser Glu Val Arg Gly Tyr Leu Leu Asp Arg Glu Gln Ile Asn
405 410 415

<210> 154

<211> 277

<212> PRT

<213> Streptococcus pneumoniae

<400> 154

Val Gly Ile Arg Val Tyr Lys Pro Thr Thr Asn Gly Arg Arg Asn Met
1 5 10 15

Thr Ser Leu Asp Phe Ala Glu Ile Thr Thr Ser Thr Pro Glu Lys Ser
20 25 30

Leu Leu Val Ala Leu Lys Ser Lys Ala Gly Arg Asn Asn Asn Gly Arg
35 40 45

Ile Thr Val Arg His Gln Gly Gly Gly His Lys Arg Phe Tyr Arg Leu
50 55 60

Val Asp Phe Lys Arg Asn Lys Asp Asn Val Glu Ala Val Val Lys Thr
65 70 75 80

Ile Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val His Tyr
85 90 95

Thr Asp Gly Val Lys Ala Tyr Ile Ile Ala Pro Lys Gly Leu Glu Val
100 105 110

Gly Gln Arg Ile Val Ser Gly Pro Glu Ala Asp Ile Lys Val Gly Asn
115 120 125

Ala Leu Pro Leu Ala Asn Ile Pro Val Gly Thr Leu Ile His Asn Ile
130 135 140

Glu Leu Lys Pro Gly Arg Gly Gly Glu Leu Val Arg Ala Ala Gly Ala
145 150 155 160

Ser Ala Gln Val Leu Gly Ser Glu Gly Lys Tyr Val Leu Val Arg Leu
165 170 175

Gln Ser Gly Glu Val Arg Met Ile Leu Gly Thr Cys Arg Ala Thr Val
180 185 190

Gly Val Val Gly Asn Glu Gln His Gly Leu Val Asn Leu Gly Lys Ala
195 200 205

Gly Arg Ser Arg Trp Lys Gly Ile Arg Pro Thr Val Arg Gly Ser Val
210 215 220

Met Asn Pro Asn Asp His Pro His Gly Gly Gly Glu Gly Lys Ala Pro
225 230 235 240

Val Gly Arg Lys Ala Pro Ser Thr Pro Trp Gly Lys Pro Ala Leu Gly
245 250 255

Leu Lys Thr Arg Asn Lys Lys Ala Lys Ser Asp Lys Leu Ile Val Arg
260 265 270

Arg Arg Asn Glu Lys
275

<210> 155

<211> 89

<212> PRT

<213> Streptococcus pneumoniae

<400> 155

Met Ala Lys Lys Ser Met Val Ala Arg Glu Ala Lys Arg Gln Lys Ile
1 5 10 15

Val Asp Arg Tyr Ala Glu Lys Arg Ala Ala Leu Lys Ala Ala Gly Asp
20 25 30

Tyr Glu Gly Leu Ser Lys Leu Pro Arg Asn Ala Ser Pro Thr Arg Leu
35 40 45

His Asn Arg Cys Arg Val Thr Gly Arg Pro His Ser Val Tyr Arg Lys
50 55 60

Phe Gly Leu Ser Arg Ile Ala Phe Arg Glu Leu Ala His Lys Gly Gln
65 70 75 80

Ile Pro Gly Val Thr Lys Ala Ser Trp
85

<210> 156

<211> 445

<212> PRT

<213> Streptococcus pneumoniae

<400> 156

Met Asp Ile Arg Gln Val Thr Glu Thr Ile Ala Met Ile Glu Glu Gln
1 5 10 15

Asn Phe Asp Ile Arg Thr Ile Thr Met Gly Ile Ser Leu Leu Asp Cys
20 25 30

Ile Asp Pro Asp Ile Asn Arg Ala Ala Glu Lys Ile Tyr Gln Lys Ile
35 40 45

Thr Thr Lys Ala Ala Asn Leu Val Ala Val Gly Asp Glu Ile Ala Ala
50 55 60

Glu Leu Gly Ile Pro Ile Val Asn Lys Arg Val Ser Val Thr Pro Ile
65 70 75 80

Ser Leu Ile Gly Ala Ala Thr Asp Ala Thr Asp Tyr Val Val Leu Ala
85 90 95

Lys Ala Leu Asp Lys Ala Ala Lys Glu Ile Gly Val Asp Phe Ile Gly
100 105 110

Gly Phe Ser Ala Leu Val Gln Lys Gly Tyr Gln Lys Gly Asp Glu Ile
115 120 125

Leu Ile Asn Ser Ile Pro Arg Ala Leu Ala Glu Thr Asp Lys Val Cys
130 135 140

Ser Ser Val Asn Ile Gly Ser Thr Lys Ser Gly Ile Asn Met Thr Ala
145 150 155 160

Val Ala Asp Met Gly Arg Ile Ile Lys Glu Thr Ala Asn Leu Ser Asp
165 170 175

Met Gly Val Ala Lys Leu Val Val Phe Ala Asn Ala Val Glu Asp Asn
180 185 190

Pro Phe Met Ala Gly Ala Phe His Gly Val Gly Glu Ala Asp Val Ile
195 200 205

Ile Asn Val Gly Val Ser Gly Pro Gly Val Val Lys Arg Ala Leu Glu
210 215 220

Lys Val Arg Gly Gln Ser Phe Asp Val Val Ala Glu Thr Val Lys Lys
225 230 235 240

Thr Ala Phe Lys Ile Thr Arg Ile Gly Gln Leu Val Gly Gln Met Ala
245 250 255

Ser Glu Arg Leu Gly Val Glu Phe Gly Ile Val Asp Leu Ser Leu Ala
260 265 270

Pro Thr Pro Ala Val Gly Asp Ser Val Ala Arg Val Leu Glu Glu Met
275 280 285

Gly Leu Glu Thr Val Gly Thr His Gly Thr Thr Ala Ala Leu Ala Leu
290 295 300

Leu Asn Asp Gln Val Lys Lys Gly Gly Val Met Ala Cys Asn Gln Val
305 310 315 320

Gly Gly Leu Ser Gly Ala Phe Ile Pro Val Ser Glu Asp Glu Gly Met
325 330 335

Ile Ala Ala Val Gln Asn Gly Ser Leu Asn Leu Glu Lys Leu Glu Ala
340 345 350

Met Thr Ala Ile Cys Ser Val Gly Leu Asp Met Ile Ala Ile Pro Glu
355 360 365

Asp Thr Pro Ala Glu Thr Ile Ala Ala Met Ile Ala Asp Glu Ala Ala
370 375 380

Ile Gly Val Ile Asn Met Lys Thr Thr Ala Val Arg Ile Ile Pro Lys
385 390 395 400

Gly Lys Glu Gly Asp Met Ile Glu Phe Gly Gly Leu Leu Gly Thr Ala
405 410 415

Pro Val Met Lys Val Asn Gly Ala Ser Ser Val Asp Phe Ile Ser Arg
420 425 430

Gly Gly Gln Ile Pro Ala Pro Ile His Ser Phe Lys Asn
435 440 445

<210> 157

<211> 812

<212> PRT

<213> Streptococcus pneumoniae

<400> 157

Met Val Asn Thr Glu Val Ala Arg Thr Thr Ile Lys Thr Glu Tyr Phe
1 5 10 15

Gly Ser Leu Thr Glu Arg Met Asn Lys Tyr Arg Glu Asp Val Leu Asn
20 25 30

Lys Lys Pro Tyr Ile Asp Ala Glu Arg Ala Val Leu Ala Thr Arg Ala
35 40 45

Tyr Glu Arg Tyr Lys Glu Gln Pro Asn Val Leu Lys Arg Ala Tyr Met
50 55 60

Leu Lys Glu Ile Leu Glu Asn Met Thr Ile Tyr Ile Glu Glu Glu Ser
65 70 75 80

Met Ile Ala Gly Asn Gln Ala Ser Ser Asn Lys Asp Ala Pro Ile Phe
85 90 95

Pro Glu Tyr Thr Leu Glu Phe Val Leu Asn Glu Leu Asp Leu Phe Glu
100 105 110

Lys Arg Asp Gly Asp Val Phe Tyr Ile Thr Glu Glu Thr Lys Glu Gln
115 120 125

Leu Arg Ser Ile Ala Pro Phe Trp Glu Asn Asn Asn Leu Arg Ala Arg
130 135 140

Ala Gly Ala Leu Leu Pro Glu Glu Val Ser Val Tyr Met Glu Thr Gly
145 150 155 160

Phe Phe Gly Met Glu Gly Lys Met Asn Ser Gly Asp Ala His Leu Ala
165 170 175

Val Asn Tyr Gln Lys Leu Leu Gln Phe Gly Leu Arg Gly Phe Glu Glu
180 185 190

Arg Ala Arg Lys Ala Lys Val Ala Leu Asp Leu Thr Asp Pro Ala Ser
195 200 205

Ile Asp Lys Tyr His Phe Tyr Asp Ser Ile Phe Ile Val Ile Asp Ala
210 215 220

Ile Lys Val Tyr Ala Lys Arg Phe Val Ala Leu Ala Lys Ser Leu Ala
225 230 235 240

Glu Asn Ala Asn Pro Lys Arg Lys Lys Glu Leu Leu Glu Ile Ala Asp
245 250 255

Ile Cys Ser Arg Val Pro Tyr Glu Pro Ala Thr Thr Phe Ala Glu Ala
260 265 270

Ile Gln Ser Val Trp Phe Ile Gln Cys Ile Leu Gln Ile Glu Ser Asn
275 280 285

Gly His Ser Leu Ser Tyr Gly Arg Phe Asp Gln Tyr Met Tyr Pro Tyr
290 295 300

Met Lys Ala Asp Leu Glu Ser Gly Lys Glu Thr Glu Asp Ser Ile Val
305 310 315 320

Glu Arg Leu Thr Asn Leu Trp Ile Lys Thr Ile Thr Ile Asn Lys Val
325 330 335

Arg Ser Gln Ser His Thr Phe Ser Ser Ala Gly Ser Pro Leu Tyr Gln
340 345 350

Asn Val Thr Ile Gly Gly Gln Thr Arg Asp Lys Lys Asp Ala Val Asn
355 360 365

Pro Leu Ser Tyr Leu Val Leu Lys Ser Val Ala Gln Thr His Leu Pro
370 375 380

Gln Pro Asn Leu Thr Val Arg Tyr His Ala Gly Leu Asp Ala Arg Phe
385 390 395 400

Met Asn Glu Cys Ile Glu Val Met Lys Leu Gly Phe Gly Met Pro Ala
405 410 415

Phe Asn Asn Asp Glu Ile Ile Ile Pro Ser Phe Ile Ala Lys Gly Val
420 425 430

Leu Glu Asp Asp Ala Tyr Asp Tyr Ser Ala Ile Gly Cys Val Glu Thr
435 440 445

Ala Val Pro Gly Lys Trp Gly Tyr Arg Cys Thr Gly Met Ser Tyr Met
450 455 460

Asn Phe Pro Lys Val Leu Leu Ile Thr Met Asn Asp Gly Ile Asp Pro
465 470 475 480

Ala Ser Gly Lys Arg Phe Ala Pro Ser Phe Gly Arg Phe Lys Asp Met
485 490 495

Lys Asn Phe Ser Glu Leu Glu Asn Ala Trp Asp Lys Thr Leu Arg Tyr
500 505 510

Leu Thr Arg Met Ser Val Ile Val Glu Asn Ser Ile Asp Leu Ser Leu
515 520 525

Glu Arg Glu Val Pro Asp Ile Leu Cys Ser Ala Leu Thr Asp Asp Cys
530 535 540

Ile Gly Arg Gly Lys His Leu Lys Glu Gly Gly Ala Val Tyr Asp Tyr
545 550 555 560

Ile Ser Gly Leu Gln Val Gly Ile Ala Asn Leu Ser Asp Ser Leu Ala
565 570 575

Ala Ile Lys Lys Leu Val Phe Glu Glu Glu Arg Ile Ser Pro Ser Gln
580 585 590

Leu Trp His Ala Leu Glu Thr Asp Tyr Ala Gly Glu Glu Gly Lys Val
595 600 605

Ile Gln Glu Met Leu Ile His Asp Ala Pro Lys Tyr Gly Asn Asp Asp
610 615 620

Asp Tyr Ala Asp Lys Leu Val Thr Ala Ala Tyr Asp Ile Tyr Val Asp
625 630 635 640

Glu Ile Ala Lys Tyr Pro Asn Thr Arg Tyr Gly Arg Gly Pro Ile Gly
645 650 655

Gly Ile Arg Tyr Ser Gly Thr Ser Ser Ile Ser Ala Asn Val Gly Gln
660 665 670

Gly Arg Gly Thr Leu Ala Thr Pro Asp Gly Arg Asn Ala Gly Thr Pro
675 680 685

Leu Ala Glu Gly Cys Ser Pro Ser His Asn Met Asp Gln His Gly Pro
690 695 700

Thr Ser Val Leu Lys Ser Val Ser Lys Leu Pro Thr Asp Glu Ile Val
705 710 715 720

Gly Gly Val Leu Leu Asn Gln Lys Val Asn Pro Gln Thr Leu Ala Lys
725 730 735

Glu Glu Asp Lys Leu Lys Leu Ile Ala Leu Leu Arg Thr Phe Phe Asn
740 745 750

Arg Leu His Gly Tyr His Ile Gln Tyr Asn Val Val Ser Arg Glu Thr
755 760 765

Leu Ile Asp Ala Gln Lys His Pro Glu Lys His Arg Asp Leu Ile Val
770 775 780

Arg Val Ala Gly Tyr Ser Ala Phe Phe Asn Val Leu Ser Lys Ala Thr
785 790 795 800

Gln Asp Asp Ile Ile Gly Arg Thr Glu His Thr Leu
805 810

<210> 158

<211> 130

<212> PRT

<213> Streptococcus pneumoniae

<400> 158

Met Ser Gln Ala Gln Tyr Ala Gly Thr Gly Arg Arg Lys Asn Ala Val
1 5 10 15

Ala Arg Val Arg Leu Val Pro Gly Thr Gly Lys Ile Thr Val Asn Lys
20 25 30

Lys Asp Val Glu Glu Tyr Ile Pro His Ala Asp Leu Arg Leu Val Ile
35 40 45

Asn Gln Pro Phe Ala Val Thr Ser Thr Val Gly Ser Tyr Asp Val Phe
50 55 60

Val Asn Val Ile Gly Gly Gly Tyr Ala Gly Gln Ser Gly Ala Ile Arg
65 70 75 80

His Gly Ile Ala Arg Ala Leu Leu Gln Val Asp Pro Asp Phe Arg Asp
85 90 95

Ser Leu Lys Arg Ala Gly Leu Leu Thr Arg Asp Ser Arg Lys Val Glu
100 105 110

Arg Lys Lys Pro Gly Leu Lys Lys Ala Arg Lys Ala Ser Gln Phe Ser
115 120 125

Lys Arg
130

<210> 159

<211> 333

<212> PRT

<213> Streptococcus pneumoniae

<400> 159

Leu Glu Lys Lys Leu Thr Ile Lys Asp Ile Ala Glu Met Ala Gln Thr
1   5   10   15

Ser Lys Thr Thr Val Ser Phe Tyr Leu Asn Gly Lys Tyr Glu Lys Met
            20   25   30

Ser Gln Glu Thr Arg Glu Lys Ile Glu Lys Val Ile His Glu Thr Asn
        35   40   45

Tyr Lys Pro Ser Ile Val Ala Arg Ser Leu Asn Ser Lys Arg Thr Lys
    50   55   60

Leu Ile Gly Val Leu Ile Gly Asp Ile Thr Asn Ser Phe Ser Asn Gln
65   70   75   80

Ile Val Lys Gly Ile Glu Asp Ile Ala Ser Gln Asn Gly Tyr Gln Val
                85   90   95

Met Ile Gly Asn Ser Asn Tyr Ser Gln Glu Ser Glu Asp Arg Tyr Ile
            100   105   110

Glu Ser Met Leu Leu Leu Gly Val Asp Gly Phe Ile Ile Gln Pro Thr
        115   120   125

Ser Asn Phe Arg Lys Tyr Ser Arg Ile Ile Asp Glu Lys Lys Lys Lys
    130   135   140

Met Val Phe Phe Asp Ser Gln Leu Tyr Glu His Arg Thr Ser Trp Val
145   150   155   160

Lys Thr Asn Asn Tyr Asp Ala Val Tyr Asp Met Thr Gln Ser Cys Ile
                165   170   175

Glu Lys Gly Tyr Glu His Phe Leu Leu Ile Thr Ala Asp Thr Ser Arg
            180   185   190

Leu Ser Thr Arg Ile Glu Arg Ala Ser Gly Phe Val Asp Ala Leu Thr
        195   200   205

Asp Ala Asn Met Arg His Ala Ser Leu Thr Ile Glu Asp Lys His Thr
    210   215   220

Asn Leu Glu Gln Ile Lys Glu Phe Leu Gln Lys Glu Ile Asp Pro Asp
225   230   235   240

Glu Lys Thr Leu Val Phe Ile Pro Asn Cys Trp Ala Leu Pro Leu Val
                245   250   255

Phe Thr Val Ile Lys Glu Leu Asn Tyr Asn Leu Pro Gln Val Gly Leu
            260   265   270

Ile Gly Phe Asp Asn Thr Glu Trp Thr Cys Phe Ser Ser Pro Ser Val
275 280 285

Ser Thr Leu Val Gln Pro Ser Phe Glu Glu Gly Gln Gln Ala Thr Lys
290 295 300

Ile Leu Ile Asp Gln Ile Glu Gly Arg Asn Gln Glu Glu Arg Gln Gln
305 310 315 320

Val Leu Asp Cys Ser Val Asn Trp Lys Glu Ser Thr Phe
325 330

<210> 160

<211> 1767

<212> PRT

<213> Streptococcus pneumoniae

<400> 160

Met Asn Lys Gly Leu Phe Glu Lys Arg Cys Lys Tyr Ser Ile Arg Lys
1 5 10 15

Phe Ser Leu Gly Val Ala Ser Val Met Ile Gly Ala Ala Phe Phe Gly
20 25 30

Thr Ser Pro Val Leu Ala Asp Ser Val Gln Ser Gly Ser Thr Ala Asn
35 40 45

Leu Pro Ala Asp Leu Ala Thr Ala Leu Ala Thr Ala Lys Glu Asn Asp
50 55 60

Gly Arg Asp Phe Glu Ala Pro Lys Val Gly Glu Asp Gln Gly Ser Pro
65 70 75 80

Glu Val Thr Asp Gly Pro Lys Thr Glu Glu Glu Leu Leu Ala Leu Glu
85 90 95

Lys Glu Lys Pro Ala Glu Glu Lys Pro Lys Glu Asp Lys Pro Ala Ala
100 105 110

Ala Lys Pro Glu Thr Pro Lys Thr Val Thr Pro Glu Trp Gln Thr Val
115 120 125

Ala Asn Lys Glu Gln Gln Gly Thr Val Thr Ile Arg Glu Glu Lys Gly
130 135 140

Val Arg Tyr Asn Gln Leu Ser Ser Thr Ala Gln Asn Asp Asn Ala Gly
145 150 155 160

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Lys Pro Ala Leu Phe Glu Lys Lys Gly Leu Thr Val Asp Ala Asn Gly
                165                 170                 175

Asn Ala Thr Val Asp Leu Thr Phe Lys Asp Asp Ser Glu Lys Gly Lys
            180                 185                 190

Ser Arg Phe Gly Val Phe Leu Lys Phe Lys Asp Thr Lys Asn Asn Val
        195                 200                 205

Phe Val Gly Tyr Asp Lys Asp Gly Trp Phe Trp Glu Tyr Lys Ser Pro
    210                 215                 220

Thr Thr Ser Thr Trp Tyr Arg Gly Ser Arg Val Ala Ala Pro Glu Thr
225                 230                 235                 240

Gly Ser Thr Asn Arg Leu Ser Ile Thr Leu Lys Ser Asp Gly Gln Leu
                245                 250                 255

Asn Ala Ser Asn Asn Asp Val Asn Leu Phe Asp Thr Val Thr Leu Pro
            260                 265                 270

Ala Ala Val Asn Asp His Leu Lys Asn Glu Lys Lys Ile Leu Leu Lys
        275                 280                 285

Ala Gly Ser Tyr Asp Asp Glu Arg Thr Val Val Ser Val Lys Thr Asp
    290                 295                 300

Asn Gln Glu Gly Val Lys Thr Glu Asp Thr Pro Ala Glu Lys Glu Thr
305                 310                 315                 320

Gly Pro Glu Val Asp Asp Ser Lys Val Thr Tyr Asp Thr Ile Gln Ser
                325                 330                 335

Lys Val Leu Lys Ala Val Ile Asp Gln Ala Phe Pro Arg Val Lys Glu
            340                 345                 350

Tyr Ser Leu Asn Gly His Thr Leu Pro Gly Gln Val Gln Gln Phe Asn
        355                 360                 365

Gln Val Phe Ile Asn Asn His Arg Ile Thr Pro Glu Val Thr Tyr Lys
    370                 375                 380

Lys Ile Asn Glu Thr Thr Ala Glu Tyr Leu Met Lys Leu Arg Asp Asp
385                 390                 395                 400

Ala His Leu Ile Asn Ala Glu Met Thr Val Arg Leu Gln Val Val Asp
                405                 410                 415

Asn Gln Leu His Phe Asp Val Thr Lys Ile Val Asn His Asn Gln Val
            420                 425                 430
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Thr Pro Gly Gln Lys Ile Asp Asp Glu Ser Lys Leu Leu Ser Ser Ile
435 440 445

Ser Phe Leu Gly Asn Ala Leu Val Ser Val Ser Ser Asn Gln Thr Gly
450 455 460

Ala Lys Phe Asp Gly Ala Thr Met Ser Asn Asn Thr His Val Ser Gly
465 470 475 480

Asp Asp His Ile Asp Val Thr Asn Pro Met Lys Asp Leu Ala Lys Gly
485 490 495

Tyr Met Tyr Gly Phe Val Ser Thr Asp Lys Leu Ala Ala Gly Val Trp
500 505 510

Ser Asn Ser Gln Asn Ser Tyr Gly Gly Gly Ser Asn Asp Trp Thr Arg
515 520 525

Leu Thr Ala Tyr Lys Glu Thr Val Gly Asn Ala Asn Tyr Val Gly Ile
530 535 540

His Ser Ser Glu Trp Gln Trp Glu Lys Ala Tyr Lys Gly Ile Val Phe
545 550 555 560

Pro Glu Tyr Thr Lys Glu Leu Pro Ser Ala Lys Val Val Ile Thr Glu
565 570 575

Asp Ala Asn Ala Asp Lys Asn Val Asp Trp Gln Asp Gly Ala Ile Ala
580 585 590

Tyr Arg Ser Ile Met Asn Asn Pro Gln Gly Trp Glu Lys Val Lys Asp
595 600 605

Ile Thr Ala Tyr Arg Ile Ala Met Asn Phe Gly Ser Gln Ala Gln Asn
610 615 620

Pro Phe Leu Met Thr Leu Asp Gly Ile Lys Lys Ile Asn Leu His Thr
625 630 635 640

Asp Gly Leu Gly Gln Gly Val Leu Leu Lys Gly Tyr Gly Ser Glu Gly
645 650 655

His Asp Ser Gly His Leu Asn Tyr Ala Asp Ile Gly Lys Arg Ile Gly
660 665 670

Gly Val Glu Asp Phe Lys Thr Leu Ile Glu Lys Ala Lys Lys Tyr Gly
675 680 685

Ala His Leu Gly Ile His Val Asn Ala Ser Glu Thr Tyr Pro Glu Ser
690 695 700

Lys Tyr Phe Asn Glu Lys Ile Leu Arg Lys Asn Pro Asp Gly Ser Tyr
705 710 715 720

Ser Tyr Gly Trp Asn Trp Leu Asp Gln Gly Ile Asn Ile Asp Ala Ala
725 730 735

Tyr Asp Leu Ala His Gly Arg Leu Ala Arg Trp Glu Asp Leu Lys Lys
740 745 750

Lys Leu Gly Asp Gly Leu Asp Phe Ile Tyr Val Asp Val Trp Gly Asn
755 760 765

Gly Gln Ser Gly Asp Asn Gly Ala Trp Ala Thr His Val Leu Ala Lys
770 775 780

Glu Ile Asn Lys Gln Gly Trp Arg Phe Ala Ile Glu Trp Gly His Gly
785 790 795 800

Gly Glu Tyr Asp Ser Thr Phe His His Trp Ala Ala Asp Leu Thr Tyr
805 810 815

Gly Gly Tyr Thr Asn Lys Gly Ile Asn Ser Ala Ile Thr Arg Phe Ile
820 825 830

Arg Asn His Gln Lys Asp Ala Trp Val Gly Asp Tyr Arg Ser Tyr Gly
835 840 845

Gly Ala Ala Asn Tyr Pro Leu Leu Gly Gly Tyr Ser Met Lys Asp Phe
850 855 860

Glu Gly Trp Gln Gly Arg Ser Asp Tyr Asn Gly Tyr Val Thr Asn Leu
865 870 875 880

Phe Ala His Asp Val Met Thr Lys Tyr Phe Gln His Phe Thr Val Ser
885 890 895

Lys Trp Glu Asn Gly Thr Pro Val Thr Met Thr Asp Asn Gly Ser Thr
900 905 910

Tyr Lys Trp Thr Pro Glu Met Arg Val Glu Leu Val Asp Ala Asp Asn
915 920 925

Asn Lys Val Val Val Thr Arg Lys Ser Asn Asp Val Asn Ser Pro Gln
930 935 940

Tyr Arg Glu Arg Thr Val Thr Leu Asn Gly Arg Val Ile Gln Asp Gly
945 950 955 960

Ser Ala Tyr Leu Thr Pro Trp Asn Trp Asp Ala Asn Gly Lys Lys Leu
965 970 975

Ser Thr Asp Lys Glu Lys Met Tyr Tyr Phe Asn Thr Gln Ala Gly Ala
980 985 990

Thr Thr Trp Thr Leu Pro Ser Asp Trp Ala Lys Ser Lys Val Tyr Leu
995 1000 1005

Tyr Lys Leu Thr Asp Gln Gly Lys Thr Glu Glu Gln Glu Leu Thr
1010 1015 1020

Val Lys Asp Gly Lys Ile Thr Leu Asp Leu Leu Ala Asn Gln Pro
1025 1030 1035

Tyr Val Leu Tyr Arg Ser Lys Gln Thr Asn Pro Glu Met Ser Trp
1040 1045 1050

Ser Glu Gly Met His Ile Tyr Asp Gln Gly Phe Asn Ser Gly Thr
1055 1060 1065

Leu Lys His Trp Thr Ile Ser Gly Asp Ala Ser Lys Ala Glu Ile
1070 1075 1080

Val Lys Ser Gln Gly Ala Asn Asp Met Leu Arg Ile Gln Gly Asn
1085 1090 1095

Lys Glu Lys Val Ser Leu Thr Gln Lys Leu Thr Gly Leu Lys Pro
1100 1105 1110

Asn Thr Lys Tyr Ala Val Tyr Val Gly Val Asp Asn Arg Ser Asn
1115 1120 1125

Ala Lys Ala Ser Ile Thr Val Asn Thr Gly Glu Lys Glu Val Thr
1130 1135 1140

Thr Tyr Thr Asn Lys Ser Leu Ala Leu Asn Tyr Val Lys Ala Tyr
1145 1150 1155

Ala His Asn Thr Arg Arg Asp Asn Ala Thr Val Asp Asp Thr Ser
1160 1165 1170

Tyr Phe Gln Asn Met Tyr Ala Phe Phe Thr Thr Gly Ala Asp Val
1175 1180 1185

Ser Asn Val Thr Leu Thr Leu Ser Arg Glu Ala Gly Asp Gln Ala
1190 1195 1200

Thr Tyr Phe Asp Glu Ile Arg Thr Phe Glu Asn Asn Ser Ser Met
1205 1210 1215

Tyr Gly Asp Lys His Asp Thr Gly Lys Gly Thr Phe Lys Gln Asp
1220 1225 1230

Phe Glu Asn Val Ala Gln Gly Ile Phe Pro Phe Val Val Gly Gly
1235 1240 1245

Val Glu Gly Val Glu Asp Asn Arg Thr His Leu Ser Glu Lys His
1250 1255 1260

Asn Pro Tyr Thr Gln Arg Gly Trp Asn Gly Lys Lys Val Asp Asp
1265 1270 1275

Val Ile Glu Gly Asn Trp Ser Leu Lys Thr Asn Gly Leu Val Ser
1280 1285 1290

Arg Arg Asn Leu Val Tyr Gln Thr Ile Pro Gln Asn Phe Arg Phe
1295 1300 1305

Glu Ala Gly Lys Thr Tyr Arg Val Thr Phe Glu Tyr Glu Ala Gly
1310 1315 1320

Ser Asp Asn Thr Tyr Ala Phe Val Val Gly Lys Gly Glu Phe Gln
1325 1330 1335

Ser Gly Arg Arg Gly Thr Gln Ala Ser Asn Leu Glu Met His Glu
1340 1345 1350

Leu Pro Asn Thr Trp Thr Asp Ser Lys Lys Ala Lys Lys Ala Thr
1355 1360 1365

Phe Leu Val Thr Gly Ala Glu Thr Gly Asp Thr Trp Val Gly Ile
1370 1375 1380

Tyr Ser Thr Gly Asn Ala Ser Asn Thr Arg Gly Asp Ser Gly Gly
1385 1390 1395

Asn Ala Asn Phe Arg Gly Tyr Asn Asp Phe Met Met Asp Asn Leu
1400 1405 1410

Gln Ile Glu Glu Ile Thr Leu Thr Gly Lys Met Leu Thr Glu Asn
1415 1420 1425

Ala Leu Lys Asn Tyr Leu Pro Thr Val Ala Met Thr Asn Tyr Thr
1430 1435 1440

Lys Glu Ser Met Asp Ala Leu Lys Glu Ala Val Phe Asn Leu Ser
1445 1450 1455

Gln Ala Asp Asp Asp Ile Ser Val Glu Glu Ala Arg Ala Glu Ile
1460 1465 1470

Ala Lys Ile Glu Ala Leu Lys Asn Ala Leu Val Gln Lys Lys Thr
1475 1480 1485

Ala Leu Val Ala Asp Asp Phe Ala Ser Leu Thr Ala Pro Ala Gln
1490 1495 1500

Ala Gln Glu Gly Leu Ala Asn Ala Phe Asp Gly Asn Val Ser Ser
1505 1510 1515

Leu Trp His Thr Ser Trp Asn Gly Gly Asp Val Gly Lys Pro Ala
1520 1525 1530

Thr Met Val Leu Lys Glu Pro Thr Glu Ile Thr Gly Leu Arg Tyr
1535 1540 1545

Val Pro Arg Gly Ser Gly Ser Asn Gly Asn Leu Arg Asp Val Lys
1550 1555 1560

Leu Val Val Thr Asp Glu Ser Gly Lys Glu His Thr Phe Thr Ala
1565 1570 1575

Thr Asp Trp Pro Asn Asn Asn Lys Pro Lys Asp Ile Asp Phe Gly
1580 1585 1590

Lys Thr Ile Lys Ala Lys Lys Ile Val Leu Thr Gly Thr Lys Thr
1595 1600 1605

Tyr Gly Asp Gly Gly Asp Lys Tyr Gln Ser Ala Ala Glu Leu Ile
1610 1615 1620

Phe Thr Arg Pro Gln Val Ala Glu Thr Pro Leu Asp Leu Ser Gly
1625 1630 1635

Tyr Glu Ala Ala Leu Val Lys Ala Gln Lys Leu Thr Asp Lys Asp
1640 1645 1650

Asn Gln Glu Glu Val Ala Ser Val Gln Ala Ser Met Lys Tyr Ala
1655 1660 1665

Thr Asp Asn His Leu Leu Thr Glu Arg Met Val Glu Tyr Phe Ala
1670 1675 1680

Asp Tyr Leu Asn Gln Leu Lys Asp Ser Ala Thr Lys Pro Asp Ala
1685 1690 1695

Pro Thr Val Glu Lys Pro Glu Phe Lys Leu Arg Ser Leu Ala Ser
1700 1705 1710

Glu Gln Gly Lys Thr Pro Asp Tyr Lys Gln Glu Ile Ala Arg Pro
1715 1720 1725

Glu Thr Pro Glu Gln Ile Leu Pro Ala Thr Gly Glu Ser Gln Ser
1730 1735 1740

Asp Thr Ala Leu Ile Leu Ala Ser Val Ser Leu Ala Leu Ser Ala
1745 1750 1755

Leu Phe Val Val Lys Thr Lys Lys Asp
1760 1765

<210> 161

<211> 719

<212> PRT

<213> Streptococcus pneumoniae

<400> 161

Met Asn Lys Pro Thr Ile Leu Arg Leu Ile Lys Tyr Leu Ser Ile Ser
1 5 10 15

Phe Leu Ser Leu Val Ile Ala Ala Ile Val Leu Gly Gly Gly Val Phe
20 25 30

Phe Tyr Tyr Val Ser Lys Ala Pro Ser Leu Ser Glu Ser Lys Leu Val
35 40 45

Ala Thr Thr Ser Ser Lys Ile Tyr Asp Asn Lys Asn Gln Leu Ile Ala
50 55 60

Asp Leu Gly Ser Glu Arg Arg Val Asn Ala Gln Ala Asn Asp Ile Pro
65 70 75 80

Thr Asp Leu Val Lys Ala Ile Val Ser Ile Glu Asp His Arg Phe Phe
85 90 95

Asp His Arg Gly Ile Asp Thr Ile Arg Ile Leu Gly Ala Phe Leu Arg
100 105 110

Asn Leu Gln Ser Asn Ser Leu Gln Gly Gly Ser Thr Leu Thr Gln Gln
115 120 125

Leu Ile Lys Leu Thr Tyr Phe Ser Thr Ser Thr Ser Asp Gln Thr Ile
130 135 140

Ser Arg Lys Ala Gln Glu Ala Trp Leu Ala Ile Gln Leu Glu Gln Lys
145 150 155 160

Ala Thr Lys Gln Glu Ile Leu Thr Tyr Tyr Ile Asn Lys Val Tyr Met
165 170 175

Ser Asn Gly Asn Tyr Gly Met Gln Thr Ala Ala Gln Asn Tyr Tyr Gly
180 185 190

Lys Asp Leu Asn Asn Leu Ser Leu Pro Gln Leu Ala Leu Leu Ala Gly
195 200 205

Met Pro Gln Ala Pro Asn Gln Tyr Asp Pro Tyr Ser His Pro Glu Ala
210 215 220

Ala Gln Asp Arg Arg Asn Leu Val Leu Ser Glu Met Lys Asn Gln Gly
225 230 235 240

Tyr Ile Ser Ala Glu Gln Tyr Glu Lys Ala Val Asn Thr Pro Ile Thr
245 250 255

Asp Gly Leu Gln Ser Leu Lys Ser Ala Ser Asn Tyr Pro Ala Tyr Met
260 265 270

Asp Asn Tyr Leu Lys Glu Val Ile Asn Gln Val Glu Glu Glu Thr Gly
275 280 285

Tyr Asn Leu Leu Thr Thr Gly Met Asp Val Tyr Thr Asn Val Asp Gln
290 295 300

Glu Ala Gln Lys His Leu Trp Asp Ile Tyr Asn Thr Asp Glu Tyr Val
305 310 315 320

Ala Tyr Pro Asp Asp Glu Leu Gln Val Ala Ser Thr Ile Val Asp Val
325 330 335

Ser Asn Gly Lys Val Ile Ala Gln Leu Gly Ala Arg His Gln Ser Ser
340 345 350

Asn Val Ser Phe Gly Ile Asn Gln Ala Val Glu Thr Asn Arg Asp Trp
355 360 365

Gly Ser Thr Met Lys Pro Ile Thr Asp Tyr Ala Pro Ala Leu Glu Tyr
370 375 380

Gly Val Tyr Asp Ser Thr Ala Thr Ile Val His Asp Glu Pro Tyr Asn
385 390 395 400

Tyr Pro Gly Thr Asn Thr Pro Val Tyr Asn Trp Asp Arg Gly Tyr Phe
405 410 415

Gly Asn Ile Thr Leu Gln Tyr Ala Leu Gln Gln Ser Arg Asn Val Pro
420 425 430

Ala Val Glu Thr Leu Asn Lys Val Gly Leu Asn Arg Ala Lys Thr Phe
435 440 445

Leu Asn Gly Leu Gly Ile Asp Tyr Pro Ser Ile His Tyr Ser Asn Ala
450 455 460

Ile Ser Ser Asn Thr Thr Glu Ser Asp Lys Lys Tyr Gly Ala Ser Ser
465 470 475 480

Glu Lys Met Ala Ala Ala Tyr Ala Ala Phe Ala Asn Gly Gly Thr Tyr
485 490 495

Tyr Lys Pro Met Tyr Ile His Lys Val Val Phe Ser Asp Gly Ser Glu
500 505 510

Lys Glu Phe Ser Asn Val Gly Thr Arg Ala Met Lys Glu Thr Thr Ala
515 520 525

Tyr Met Met Thr Asp Met Met Lys Thr Val Leu Thr Tyr Gly Thr Gly
530 535 540

Arg Asn Ala Tyr Leu Ala Trp Leu Pro Gln Ala Gly Lys Thr Gly Thr
545 550 555 560

Ser Asn Tyr Thr Asp Glu Glu Ile Glu Asn His Ile Lys Thr Ser Gln
565 570 575

Phe Val Ala Pro Asp Glu Leu Phe Ala Gly Tyr Thr Arg Lys Tyr Ser
580 585 590

Met Ala Val Trp Thr Gly Tyr Ser Asn Arg Leu Thr Pro Leu Val Gly
595 600 605

Asn Gly Leu Thr Val Ala Ala Lys Val Tyr Arg Ser Met Met Thr Tyr
610 615 620

Leu Ser Glu Gly Ser Asn Pro Glu Asp Trp Asn Ile Pro Glu Gly Leu
625 630 635 640

Tyr Arg Asn Gly Glu Phe Val Phe Lys Asn Gly Ala Arg Ser Thr Trp
645 650 655

Asn Ser Pro Ala Pro Gln Gln Pro Pro Ser Thr Glu Ser Ser Ser Ser
660 665 670

Ser Ser Asp Ser Ser Thr Ser Gln Ser Ser Ser Thr Thr Pro Ser Thr
675 680 685

Asn Asn Ser Thr Thr Thr Asn Pro Asn Asn Asn Thr Gln Gln Ser Asn
690 695 700

Thr Thr Pro Asp Gln Gln Asn Gln Asn Pro Gln Pro Ala Gln Pro
705 710 715

<210> 162

<211> 464

<212> PRT

<213> Streptococcus pneumoniae

<400> 162

Met Ser Lys Lys Arg Arg Asn Arg His Lys Lys Glu Gly Gln Glu Pro
1   5   10   15

Gln Phe Asp Phe Asp Glu Ala Lys Glu Leu Thr Val Gly Gln Ala Ile
            20   25   30

Arg Lys Asn Glu Glu Val Glu Ser Gly Val Leu Pro Glu Asp Ser Ile
        35   40   45

Leu Asp Lys Tyr Val Lys Gln His Arg Asp Glu Ile Glu Ala Asp Lys
    50   55   60

Phe Ala Thr Arg Gln Tyr Lys Lys Glu Glu Phe Val Glu Thr Gln Ser
65   70   75   80

Leu Asp Asp Leu Ile Gln Glu Met Arg Glu Ala Val Glu Lys Ser Glu
                85   90   95

Ala Ser Ser Glu Glu Val Pro Ser Ser Glu Asp Ile Leu Leu Pro Leu
            100   105   110

Pro Leu Asp Asp Glu Glu Gln Gly Leu Asp Pro Leu Leu Leu Asp Asp
        115   120   125

Glu Asn Pro Thr Glu Met Thr Glu Glu Val Glu Glu Glu Gln Asn Leu
    130   135   140

Ser Arg Leu Asp Gln Glu Asp Ser Glu Lys Lys Ser Lys Lys Gly Phe
145   150   155   160

Ile Leu Thr Val Leu Ala Leu Val Ser Val Ile Ile Cys Val Ser Ala
                165   170   175

Tyr Tyr Val Tyr Arg Gln Val Ala Arg Ser Thr Lys Glu Ile Glu Thr
            180   185   190

Ser Gln Ser Thr Thr Ala Asn Gln Ser Asp Val Asp Asp Phe Asn Thr
        195   200   205

Leu Tyr Asp Ala Phe Tyr Thr Asp Ser Asn Lys Thr Ala Leu Lys Asn
    210   215   220

Ser Gln Phe Asp Lys Leu Ser Gln Leu Lys Thr Leu Leu Asp Lys Leu
225   230   235   240

Glu Gly Ser Arg Glu His Thr Leu Ala Lys Ser Lys Tyr Asp Ser Leu
245 250 255

Ala Thr Gln Ile Lys Ala Ile Gln Asp Val Asn Ala Gln Phe Glu Lys
260 265 270

Pro Ala Ile Val Asp Gly Val Leu Asp Thr Asn Ala Lys Ala Lys Ser
275 280 285

Asp Ala Lys Phe Thr Asp Ile Lys Thr Gly Asn Thr Glu Leu Asp Lys
290 295 300

Val Leu Asp Lys Ala Ile Ser Leu Gly Lys Ser Gln Gln Thr Ser Thr
305 310 315 320

Ser Ser Ser Ser Ser Ser Gln Thr Ser Ser Ser Ser Ser Ser Gln Ala
325 330 335

Ser Ser Asn Thr Thr Ser Glu Pro Lys Pro Ser Ser Ser Asn Glu Thr
340 345 350

Arg Ser Ser Arg Ser Glu Val Asn Met Gly Leu Ser Ser Ala Gly Val
355 360 365

Ala Val Gln Arg Ser Ala Ser Arg Val Ala Tyr Asn Gln Ser Ala Ile
370 375 380

Asp Asp Ser Asn Asn Ser Ala Trp Asp Phe Ala Asp Gly Val Leu Glu
385 390 395 400

Gln Ile Leu Ala Thr Ser Arg Ser Arg Gly Tyr Ile Thr Gly Asp Gln
405 410 415

Tyr Ile Leu Glu Arg Val Asn Ile Val Asn Gly Asn Gly Tyr Tyr Asn
420 425 430

Leu Tyr Lys Pro Asp Gly Thr Tyr Leu Phe Thr Leu Asn Cys Lys Thr
435 440 445

Gly Tyr Phe Val Gly Asn Gly Ala Gly His Ala Asp Asp Leu Asp Tyr
450 455 460

<210> 163

<211> 340

<212> PRT

<213> Streptococcus pneumoniae

<400> 163

Met Lys Leu Leu Lys Lys Met Met Gln Val Ala Leu Ala Val Phe Phe
1   5   10   15

Phe Gly Leu Leu Ala Thr Asn Thr Val Phe Ala Asn Thr Thr Gly Gly
            20   25   30

Arg Phe Val Asp Lys Asp Asn Arg Lys Tyr Tyr Val Lys Asp Asp His
        35   40   45

Lys Ala Ile Tyr Trp His Lys Ile Asp Gly Lys Thr Tyr Tyr Phe Gly
    50   55   60

Asp Ile Gly Glu Met Val Val Gly Trp Gln Tyr Leu Glu Ile Pro Gly
65   70   75   80

Thr Gly Tyr Arg Asp Asn Leu Phe Asp Asn Gln Pro Val Asn Glu Ile
                85   90   95

Gly Leu Gln Glu Lys Trp Tyr Tyr Phe Gly Gln Asp Gly Ala Leu Leu
            100   105   110

Glu Gln Thr Asp Lys Gln Val Leu Glu Ala Lys Thr Ser Glu Asn Thr
        115   120   125

Gly Lys Val Tyr Gly Glu Gln Tyr Pro Leu Ser Ala Glu Lys Arg Thr
    130   135   140

Tyr Tyr Phe Asp Asn Asn Tyr Ala Val Lys Thr Gly Trp Ile Tyr Glu
145   150   155   160

Glu Gly His Trp Tyr Tyr Leu Asn Lys Leu Gly Asn Phe Gly Asp Asp
                165   170   175

Ser Tyr Asn Pro Leu Pro Ile Gly Glu Val Ala Lys Gly Trp Thr Gln
            180   185   190

Asp Phe His Val Thr Ile Asp Ile Asp Arg Ser Lys Pro Ala Pro Trp
        195   200   205

Tyr Tyr Leu Asp Ala Ser Gly Lys Met Leu Thr Asp Trp Gln Lys Val
    210   215   220

Asn Gly Lys Trp Tyr Tyr Phe Gly Ser Ser Gly Ser Met Ala Thr Gly
225   230   235   240

Trp Lys Tyr Val Arg Gly Lys Trp Tyr Tyr Leu Asp Asn Lys Asn Gly
                245   250   255

Asp Met Lys Thr Gly Trp Gln Tyr Leu Gly Asn Lys Trp Tyr Tyr Leu
            260   265   270

Arg Ser Ser Gly Ala Met Val Thr Gly Trp Tyr Gln Asp Gly Ser Thr
275 280 285

Trp Tyr Tyr Leu Asp Pro Ser Asn Gly Asp Met Lys Ile Gly Trp Thr
290 295 300

Lys Val Asn Gly Lys Trp Tyr Tyr Leu Asn Ser Asn Gly Ala Met Val
305 310 315 320

Thr Gly Ser Gln Thr Ile Asp Gly Lys Val Tyr Asn Phe Ala Ser Ser
325 330 335

Gly Glu Trp Ile
340

<210> 164

<211> 332

<212> PRT

<213> Streptococcus pneumoniae

<400> 164

Met Lys Ile Leu Lys Lys Thr Met Gln Val Gly Leu Thr Val Phe Phe
1 5 10 15

Phe Gly Leu Leu Gly Thr Ser Thr Val Phe Ala Asp Asp Ser Glu Gly
20 25 30

Trp Gln Phe Val Gln Glu Asn Gly Arg Thr Tyr Tyr Lys Lys Gly Asp
35 40 45

Leu Lys Glu Thr Tyr Trp Arg Val Ile Asp Gly Lys Tyr Tyr Tyr Phe
50 55 60

Asp Ser Leu Ser Gly Glu Met Val Val Gly Trp Gln Tyr Ile Pro Phe
65 70 75 80

Pro Ser Lys Gly Ser Thr Ile Gly Pro Tyr Pro Asn Gly Ile Arg Leu
85 90 95

Glu Gly Phe Pro Lys Ser Glu Trp Tyr Tyr Phe Asp Lys Asn Gly Val
100 105 110

Leu Gln Glu Phe Val Gly Trp Lys Thr Leu Glu Ile Lys Thr Lys Asp
115 120 125

Ser Val Gly Arg Lys Tyr Gly Glu Lys Arg Glu Asp Ser Glu Asp Lys
130 135 140

Glu Glu Lys Arg Tyr Tyr Thr Asn Tyr Tyr Phe Asn Gln Asn His Ser
145 150 155 160

Leu Glu Thr Gly Trp Leu Tyr Asp Gln Ser Asn Trp Tyr Tyr Leu Ala
165 170 175

Lys Thr Glu Ile Asn Gly Glu Asn Tyr Leu Gly Gly Glu Arg Arg Ala
180 185 190

Gly Trp Ile Asn Asp Asp Ser Thr Trp Tyr Tyr Leu Asp Pro Thr Thr
195 200 205

Gly Ile Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Lys Trp Tyr Tyr
210 215 220

Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Glu Gly Thr
225 230 235 240

Thr Trp Tyr Tyr Leu Asp His Pro Asn Gly Asp Met Lys Thr Gly Trp
245 250 255

Gln Asn Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met
260 265 270

Ala Thr Gly Trp Tyr Gln Asp Gly Ser Thr Trp Tyr Tyr Leu Asn Ala
275 280 285

Gly Asn Gly Asp Met Lys Thr Gly Trp Phe Gln Val Asn Gly Asn Trp
290 295 300

Tyr Tyr Ala Tyr Ser Ser Gly Ala Leu Ala Val Asn Thr Thr Val Asp
305 310 315 320

Gly Tyr Ser Val Asn Tyr Asn Gly Glu Trp Val Arg
325 330

<210> 165

<211> 285

<212> PRT

<213> Streptococcus pneumoniae

<400> 165

Met Val Leu Ser Lys Tyr Tyr Gly Val Ala Asp Gly Met Asn Val Glu
1 5 10 15

Gly Arg Gly Ser Ala Asn Phe Ile Lys Asp Asn Val Leu Ile Thr Ala
20 25 30

Ala His Asn Tyr Tyr Arg His Asp Tyr Gly Lys Glu Ala Asp Asp Ile
35 40 45

Tyr Val Leu Pro Ala Val Ser Pro Ser Gln Glu Pro Phe Gly Lys Ile
50 55 60

Lys Val Lys Glu Val Arg Tyr Leu Lys Glu Phe Arg Asn Leu Asn Ser
65 70 75 80

Lys Asp Ala Arg Glu Tyr Asp Leu Ala Leu Leu Ile Leu Glu Glu Pro
85 90 95

Ile Gly Ala Lys Leu Gly Thr Leu Gly Leu Pro Thr Ser Gln Lys Asn
100 105 110

Leu Thr Gly Ile Thr Val Thr Ile Thr Gly Tyr Pro Ser Tyr Asn Phe
115 120 125

Lys Ile His Gln Met Tyr Thr Asp Lys Lys Gln Val Leu Ser Asp Asp
130 135 140

Gly Met Phe Leu Asp Tyr Gln Val Asp Thr Leu Glu Gly Ser Ser Gly
145 150 155 160

Ser Thr Val Tyr Asp Ala Ser His Arg Val Val Gly Val His Thr Leu
165 170 175

Gly Asp Gly Ala Asn Gln Ile Asn Ser Ala Val Lys Leu Asn Glu Arg
180 185 190

Asn Leu Pro Phe Ile Tyr Ser Val Leu Lys Gly Tyr Ser Leu Glu Gly
195 200 205

Trp Lys Lys Ile Asn Gly Ser Trp Tyr His Tyr Arg Gln His Asp Lys
210 215 220

Gln Thr Gly Trp Gln Glu Ile Asn Asp Thr Trp Tyr Tyr Leu Asp Ser
225 230 235 240

Ser Gly Lys Met Leu Thr Asp Trp Gln Lys Val Asn Gly Lys Trp Tyr
245 250 255

Tyr Leu Asn Ser Asn Gly Ala Met Val Thr Gly Ser Gln Thr Ile Asp
260 265 270

Gly Lys Val Tyr Asn Phe Ala Ser Ser Gly Glu Trp Ile
275 280 285

<210> 166

<211> 630

<212> PRT

<213> Streptococcus pneumoniae

<400> 166

Leu Met Lys Lys Thr Phe Phe Leu Leu Val Leu Gly Leu Phe Cys Leu
1 5 10 15

Leu Pro Leu Ser Val Phe Ala Ile Asp Phe Lys Ile Asn Ser Tyr Gln
20 25 30

Gly Asp Leu Tyr Ile His Ala Asp Asn Thr Ala Glu Phe Arg Gln Lys
35 40 45

Ile Val Tyr Gln Phe Glu Glu Asp Phe Lys Gly Gln Ile Val Gly Leu
50 55 60

Gly Arg Ala Gly Lys Met Pro Ser Gly Phe Asp Ile Asp Pro His Pro
65 70 75 80

Lys Ile Gln Ala Ala Lys Asn Gly Ala Glu Leu Ala Asp Val Thr Ser
85 90 95

Glu Val Thr Glu Glu Ala Asp Gly Tyr Thr Val Arg Val Tyr Asn Pro
100 105 110

Gly Gln Glu Gly Asp Ile Val Glu Val Asp Leu Val Trp Asn Leu Lys
115 120 125

Asn Leu Leu Phe Leu Tyr Asp Asp Ile Ala Glu Leu Asn Trp Gln Pro
130 135 140

Leu Thr Asp Ser Ser Glu Ser Ile Glu Lys Phe Glu Phe His Val Arg
145 150 155 160

Gly Asp Lys Gly Ala Glu Lys Leu Phe Phe His Thr Gly Lys Leu Phe
165 170 175

Arg Glu Gly Thr Ile Glu Lys Ser Asn Leu Asp Tyr Thr Ile Arg Leu
180 185 190

Asp Asn Leu Pro Ala Lys Arg Gly Val Glu Leu His Ala Tyr Trp Pro
195 200 205

Arg Thr Asp Phe Ala Ser Ala Arg Asp Gln Gly Leu Lys Gly Asn Arg
210 215 220

Leu Glu Glu Phe Asn Lys Ile Glu Asp Ser Ile Val Arg Glu Lys Asp
225 230 235 240

Gln Ser Lys Gln Leu Val Thr Trp Val Leu Pro Ser Ile Leu Ser Ile
245 250 255

Ser Leu Leu Leu Ser Val Cys Phe Tyr Phe Ile Tyr Arg Arg Lys Thr
260 265 270

Thr Pro Ser Val Lys Tyr Ala Lys Asn His Arg Leu Tyr Glu Pro Pro
275 280 285

Met Glu Leu Glu Pro Met Val Leu Ser Glu Ala Val Tyr Ser Thr Ser
290 295 300

Leu Glu Glu Val Ser Pro Leu Val Lys Gly Ala Gly Lys Phe Thr Phe
305 310 315 320

Asp Gln Leu Ile Gln Ala Thr Leu Leu Asp Val Ile Asp Arg Gly Asn
325 330 335

Val Ser Ile Ile Ser Glu Gly Asp Ala Val Gly Leu Arg Leu Val Lys
340 345 350

Glu Asp Gly Leu Ser Ser Phe Glu Lys Asp Cys Leu Asn Leu Ala Phe
355 360 365

Ser Gly Lys Lys Glu Glu Thr Leu Ser Asn Leu Phe Ala Asp Tyr Lys
370 375 380

Val Ser Asp Ser Leu Tyr Arg Arg Ala Lys Val Ser Asp Glu Lys Arg
385 390 395 400

Ile Gln Ala Arg Gly Leu Gln Leu Lys Ser Ser Phe Glu Glu Val Leu
405 410 415

Asn Gln Met Gln Glu Gly Val Arg Lys Arg Val Ser Phe Trp Gly Leu
420 425 430

Pro Asp Tyr Tyr Arg Pro Leu Thr Gly Gly Glu Lys Ala Leu Gln Val
435 440 445

Gly Met Gly Ala Leu Thr Ile Leu Pro Leu Phe Ile Gly Phe Gly Leu
450 455 460

Phe Leu Tyr Ser Leu Asp Val His Gly Tyr Leu Tyr Leu Pro Leu Pro
465 470 475 480

Ile Leu Gly Phe Leu Gly Leu Val Leu Ser Val Phe Tyr Tyr Trp Lys
485 490 495

Leu Arg Leu Asp Asn Arg Asp Gly Val Leu Asn Glu Ala Gly Ala Glu
500 505 510

Val Tyr Tyr Leu Trp Thr Ser Phe Glu Asn Met Leu Arg Glu Ile Ala
515 520 525

Arg Leu Asp Gln Ala Glu Leu Glu Ser Ile Val Val Trp Asn Arg Leu
530 535 540

Leu Val Tyr Ala Thr Leu Phe Gly Tyr Ala Asp Lys Val Ser His Leu
545 550 555 560

Met Lys Val His Gln Ile Gln Val Glu Asn Pro Asp Ile Asn Leu Tyr
565 570 575

Val Ala Tyr Gly Trp His Ser Thr Phe Tyr His Ser Thr Ala Gln Met
580 585 590

Ser His Tyr Ala Ser Val Ala Asn Thr Ala Ser Thr Tyr Ser Val Ser
595 600 605

Ser Gly Ser Gly Ser Ser Gly Gly Gly Phe Ser Gly Gly Gly Gly Gly
610 615 620

Gly Ser Ile Gly Ala Phe
625 630

<210> 167

<211> 665

<212> PRT

<213> Streptococcus pneumoniae

<400> 167

Met Lys Ser Ile Asn Lys Phe Leu Thr Met Leu Ala Ala Leu Leu Leu
1 5 10 15

Thr Ala Ser Ser Leu Phe Ser Ala Ala Thr Val Phe Ala Ala Gly Thr
20 25 30

Thr Thr Thr Ser Val Thr Val His Lys Leu Leu Ala Thr Asp Gly Asp
35 40 45

Met Asp Lys Ile Ala Asn Glu Leu Glu Thr Gly Asn Tyr Ala Gly Asn
50 55 60

Lys Val Gly Val Leu Pro Ala Asn Ala Lys Glu Ile Ala Gly Val Met
65 70 75 80

Phe Val Trp Thr Asn Thr Asn Asn Glu Ile Ile Asp Glu Asn Gly Gln
85 90 95

Thr Leu Gly Val Asn Ile Asp Pro Gln Thr Phe Lys Leu Ser Gly Ala
100 105 110

Met Pro Ala Thr Ala Met Lys Lys Leu Thr Glu Ala Glu Gly Ala Lys
115 120 125

Phe Asn Thr Ala Asn Leu Pro Ala Ala Lys Tyr Lys Ile Tyr Glu Ile
130 135 140

His Ser Leu Ser Thr Tyr Val Gly Glu Asp Gly Ala Thr Leu Thr Gly
145 150 155 160

Ser Lys Ala Val Pro Ile Glu Ile Glu Leu Pro Leu Asn Asp Val Val
165 170 175

Asp Ala His Val Tyr Pro Lys Asn Thr Glu Ala Lys Pro Lys Ile Asp
180 185 190

Lys Asp Phe Lys Gly Lys Ala Asn Pro Asp Thr Pro Arg Val Asp Lys
195 200 205

Asp Thr Pro Val Asn His Gln Val Gly Asp Val Val Glu Tyr Glu Ile
210 215 220

Val Thr Lys Ile Pro Ala Leu Ala Asn Tyr Ala Thr Ala Asn Trp Ser
225 230 235 240

Asp Arg Met Thr Glu Gly Leu Ala Phe Asn Lys Gly Thr Val Lys Val
245 250 255

Thr Val Asp Asp Val Ala Leu Glu Ala Gly Asp Tyr Ala Leu Thr Glu
260 265 270

Val Ala Thr Gly Phe Asp Leu Lys Leu Thr Asp Ala Gly Leu Ala Lys
275 280 285

Val Asn Asp Gln Asn Ala Glu Lys Thr Val Lys Ile Thr Tyr Ser Ala
290 295 300

Thr Leu Asn Asp Lys Ala Ile Val Glu Val Pro Glu Ser Asn Asp Val
305 310 315 320

Thr Phe Asn Tyr Gly Asn Asn Pro Asp His Gly Asn Thr Pro Lys Pro
325 330 335

Asn Lys Pro Asn Glu Asn Gly Asp Leu Thr Leu Thr Lys Thr Trp Val
340 345 350

Asp Ala Thr Gly Ala Pro Ile Pro Ala Gly Ala Glu Ala Thr Phe Asp
355 360 365

Leu Val Asn Ala Gln Thr Gly Lys Val Val Gln Thr Val Thr Leu Thr
370 375 380

Thr Asp Lys Asn Thr Val Thr Val Asn Gly Leu Asp Lys Asn Thr Glu
385 390 395 400

Tyr Lys Phe Val Glu Arg Ser Ile Lys Gly Tyr Ser Ala Asp Tyr Gln
405 410 415

Glu Ile Thr Thr Ala Gly Glu Ile Ala Val Lys Asn Trp Lys Asp Glu
420 425 430

Asn Pro Lys Pro Leu Asp Pro Thr Glu Pro Lys Val Val Thr Tyr Gly
435 440 445

Lys Lys Phe Val Lys Val Asn Asp Lys Asp Asn Arg Leu Ala Gly Ala
450 455 460

Glu Phe Val Ile Ala Asn Ala Asp Asn Ala Gly Gln Tyr Leu Ala Arg
465 470 475 480

Lys Ala Asp Lys Val Ser Gln Glu Glu Lys Gln Leu Val Val Thr Thr
485 490 495

Lys Asp Ala Leu Asp Arg Ala Val Ala Ala Tyr Asn Ala Leu Thr Ala
500 505 510

Gln Gln Gln Thr Gln Gln Glu Lys Glu Lys Val Asp Lys Ala Gln Ala
515 520 525

Ala Tyr Asn Ala Ala Val Ile Ala Ala Asn Asn Ala Phe Glu Trp Val
530 535 540

Ala Asp Lys Asp Asn Glu Asn Val Val Lys Leu Val Ser Asp Ala Gln
545 550 555 560

Gly Arg Phe Glu Ile Thr Gly Leu Leu Ala Gly Thr Tyr Tyr Leu Glu
565 570 575

Glu Thr Lys Gln Pro Ala Gly Tyr Ala Leu Leu Thr Ser Arg Gln Lys
580 585 590

Phe Glu Val Thr Ala Thr Ser Tyr Ser Ala Thr Gly Gln Gly Ile Glu
595 600 605

Tyr Thr Ala Gly Ser Gly Lys Asp Asp Ala Thr Lys Val Val Asn Lys
610 615 620

Lys Ile Thr Ile Pro Gln Thr Gly Gly Ile Gly Thr Ile Ile Phe Ala
625 630 635 640

Val Ala Gly Ala Ala Ile Met Gly Ile Ala Val Tyr Ala Tyr Val Lys
645 650 655

Asn Asn Lys Asp Glu Asp Gln Leu Ala
660 665

<210> 168

<211> 279

<212> PRT

<213> Streptococcus pneumoniae

<400> 168

Met Ala Val Met Ala Tyr Pro Leu Val Ser Arg Leu Tyr Tyr Arg Val
1 5 10 15

Glu Ser Asn Gln Gln Ile Ala Asp Phe Asp Lys Glu Lys Ala Thr Leu
20 25 30

Asp Glu Ala Asp Ile Asp Glu Arg Met Lys Leu Ala Gln Ala Phe Asn
35 40 45

Asp Ser Leu Asn Asn Val Val Ser Gly Asp Pro Trp Ser Glu Glu Met
50 55 60

Lys Lys Lys Gly Arg Ala Glu Tyr Ala Arg Met Leu Glu Ile His Glu
65 70 75 80

Arg Met Gly His Val Glu Ile Pro Val Ile Asp Val Asp Leu Pro Val
85 90 95

Tyr Ala Gly Thr Ala Glu Glu Val Leu Gln Gln Gly Ala Gly His Leu
100 105 110

Glu Gly Thr Ser Leu Pro Ile Gly Gly Asn Ser Thr His Ala Val Ile
115 120 125

Thr Ala His Thr Gly Leu Pro Thr Ala Lys Met Phe Thr Asp Leu Thr
130 135 140

Lys Leu Lys Val Gly Asp Lys Phe Tyr Val His Asn Ile Lys Glu Val
145 150 155 160

Met Ala Tyr Gln Val Asp Gln Val Lys Val Ile Glu Pro Thr Asn Phe
165 170 175

Asp Asp Leu Leu Ile Val Pro Gly His Asp Tyr Val Thr Leu Leu Thr
180 185 190

Cys Thr Pro Tyr Met Ile Asn Thr His Arg Leu Leu Val Arg Gly His
195 200 205

Arg Ile Pro Tyr Val Ala Glu Val Glu Glu Glu Phe Ile Ala Ala Asn
210 215 220

Lys Leu Ser His Leu Tyr Arg Tyr Leu Phe Tyr Val Ala Val Gly Leu
225 230 235 240

Ile Val Ile Leu Leu Trp Ile Ile Arg Arg Leu Arg Lys Lys Lys Lys
245 250 255

Gln Pro Glu Lys Ala Leu Lys Ala Leu Lys Ala Ala Arg Lys Glu Val
260 265 270

Lys Val Glu Asp Gly Gln Gln
275

<210> 169

<211> 283

<212> PRT

<213> Streptococcus pneumoniae

<400> 169

Met Ser Arg Thr Lys Leu Arg Ala Leu Leu Gly Tyr Leu Leu Met Leu
1 5 10 15

Val Ala Cys Leu Ile Pro Ile Tyr Cys Phe Gly Gln Met Val Leu Gln
20 25 30

Ser Leu Gly Gln Val Lys Gly His Ala Thr Phe Val Lys Ser Met Thr
35 40 45

Thr Glu Met Tyr Gln Glu Gln Gln Asn His Ser Leu Ala Tyr Asn Gln
50 55 60

Arg Leu Ala Ser Gln Asn Arg Ile Val Asp Pro Phe Leu Ala Glu Gly
65 70 75 80

Tyr Glu Val Asn Tyr Gln Val Ser Asp Asp Pro Asp Ala Val Tyr Gly
85 90 95

Tyr Leu Ser Ile Pro Ser Leu Glu Ile Met Glu Pro Val Tyr Leu Gly
100 105 110

Ala Asp Tyr His His Leu Gly Met Gly Leu Ala His Val Asp Gly Thr
115 120 125

Pro Leu Pro Leu Asp Gly Thr Gly Ile Arg Ser Val Ile Ala Gly His
130 135 140

Arg Ala Glu Pro Ser His Val Phe Phe Arg His Leu Asp Gln Leu Lys
145 150 155 160

Val Gly Asp Ala Leu Tyr Tyr Asp Asn Gly Gln Glu Ile Val Glu Tyr
165 170 175

Gln Met Met Asp Thr Glu Ile Ile Leu Pro Ser Glu Trp Glu Lys Leu
180 185 190

Glu Ser Val Ser Ser Lys Asn Ile Met Thr Leu Ile Thr Cys Asp Pro
195 200 205

Ile Pro Thr Phe Asn Lys Arg Leu Leu Val Asn Phe Glu Arg Val Ala
210 215 220

Val Tyr Gln Lys Ser Asp Pro Gln Thr Ala Ala Val Ala Arg Val Ala
225 230 235 240

Phe Thr Lys Glu Gly Gln Ser Val Ser Arg Val Ala Thr Ser Gln Trp
245 250 255

Leu Tyr Arg Gly Leu Val Val Leu Ala Phe Leu Gly Ile Leu Phe Val
260 265 270

Leu Trp Lys Leu Ala Arg Leu Leu Arg Gly Lys
275 280

<210> 170

<211> 1659

<212> PRT

<213> Streptococcus pneumoniae

<400> 170

Met Lys Asn Pro Phe Phe Glu Arg Arg Cys Arg Tyr Ser Ile Arg Lys
1 5 10 15

Leu Ser Val Gly Ala Cys Ser Leu Met Ile Gly Ala Val Leu Phe Ala
20 25 30

Gly Pro Ala Leu Ala Glu Glu Thr Ala Val Pro Glu Asn Ser Gly Ala
35 40 45

Asn Thr Glu Leu Val Ser Gly Glu Ser Glu His Ser Thr Asn Glu Ala
50 55 60

Asp Lys Gln Asn Glu Gly Glu His Ala Arg Glu Asn Lys Leu Glu Lys
65 70 75 80

Ala Glu Gly Val Ala Ile Ala Ser Glu Thr Ala Ser Pro Ala Ser Asn
85 90 95

Glu Ala Ala Thr Thr Glu Thr Ala Glu Ala Ala Ser Ala Ala Lys Pro
100 105 110

Glu Glu Lys Ala Ser Glu Val Val Ala Glu Thr Pro Ser Ala Glu Ala
115 120 125

Lys Pro Lys Ser Asp Lys Glu Thr Glu Ala Lys Pro Glu Ala Thr Asn
130 135 140

Gln Gly Asp Glu Ser Lys Pro Ala Ala Glu Ala Asn Lys Thr Glu Lys
145 150 155 160

Glu Val Gln Pro Asp Val Pro Lys Asn Thr Glu Lys Thr Leu Lys Pro
165 170 175

Lys Glu Ile Lys Phe Asn Ser Trp Glu Glu Leu Leu Lys Trp Glu Pro
180 185 190

Gly Ala Arg Glu Asp Asp Ala Ile Asn Arg Gly Ser Val Val Leu Ala
195 200 205

Ser Arg Arg Thr Gly His Leu Val Asn Glu Lys Ala Ser Lys Glu Ala
210 215 220

Lys Val Gln Ala Leu Ser Asn Thr Asn Ser Lys Ala Lys Asp His Ala
225 230 235 240

Ser Val Gly Gly Glu Glu Phe Lys Ala Tyr Ala Phe Asp Tyr Trp Gln
245 250 255

Tyr Leu Asp Ser Met Val Phe Trp Glu Gly Leu Val Pro Thr Pro Asp
260 265 270

Val Ile Asp Ala Gly His Arg Asn Gly Val Pro Val Tyr Gly Thr Leu
275 280 285

Phe Phe Asn Trp Ser Asn Ser Ile Ala Asp Gln Glu Arg Phe Ala Glu
290 295 300

Ala Leu Lys Gln Asp Ala Asp Gly Ser Phe Pro Ile Ala Arg Lys Leu
305 310 315 320

Val Asp Met Ala Lys Tyr Tyr Gly Tyr Asp Gly Tyr Phe Ile Asn Gln
325 330 335

Glu Thr Thr Gly Asp Leu Val Lys Pro Leu Gly Glu Lys Met Arg Gln
340 345 350

Phe Met Leu Tyr Ser Lys Glu Tyr Ala Ala Lys Val Asn His Pro Ile
355 360 365

Lys Tyr Ser Trp Tyr Asp Ala Met Thr Tyr Asn Tyr Gly Arg Tyr His
370 375 380

Gln Asp Gly Leu Gly Glu Tyr Asn Tyr Gln Phe Met Gln Pro Glu Gly
385 390 395 400

Asp Lys Val Pro Ala Asp Asn Phe Phe Ala Asn Phe Asn Trp Asp Lys
405 410 415

Ala Lys Asn Asp Tyr Thr Ile Ala Thr Ala Asn Trp Ile Gly Arg Asn
420 425 430

Pro Tyr Asp Val Phe Ala Gly Leu Glu Leu Gln Gln Gly Gly Ser Tyr
435 440 445

Lys Thr Lys Val Lys Trp Asn Asp Ile Leu Asp Glu Asn Gly Lys Leu
450 455 460

Arg Leu Ser Leu Gly Leu Phe Ala Pro Asp Thr Ile Thr Ser Leu Gly
465 470 475 480

Lys Thr Gly Glu Asp Tyr His Lys Asn Glu Asp Ile Phe Phe Thr Gly
485 490 495

Tyr Gln Gly Asp Pro Thr Gly Gln Lys Pro Gly Asp Lys Asp Trp Tyr
500 505 510

Gly Ile Ala Asn Leu Val Ala Asp Arg Thr Pro Ala Val Gly Asn Thr
515 520 525

Phe Thr Thr Ser Phe Asn Thr Gly His Gly Lys Lys Trp Phe Val Asp
530 535 540

Gly Lys Val Ser Lys Asp Ser Glu Trp Asn Tyr Arg Ser Val Ser Gly
545 550 555 560

Val Leu Pro Thr Trp Arg Trp Trp Gln Thr Ser Thr Gly Glu Lys Leu
565 570 575

Arg Ala Glu Tyr Asp Phe Thr Asp Ala Tyr Asn Gly Gly Asn Ser Leu
580 585 590

Lys Phe Ser Gly Asp Val Ala Gly Lys Thr Asp Gln Asp Val Arg Leu
595 600 605

Tyr Ser Thr Lys Leu Glu Val Thr Glu Lys Thr Lys Leu Arg Val Ala
610 615 620

His Lys Gly Gly Lys Gly Ser Lys Val Tyr Met Ala Phe Ser Thr Thr
625 630 635 640

Pro Asp Tyr Lys Phe Asp Asp Ala Asp Ala Trp Lys Glu Leu Thr Leu
645 650 655

Ser Asp Asn Trp Thr Asn Glu Glu Phe Asp Leu Ser Ser Leu Ala Gly
660 665 670

Lys Thr Ile Tyr Ala Val Lys Leu Phe Phe Glu His Glu Gly Ala Val
675 680 685

Lys Asp Tyr Gln Phe Asn Leu Gly Gln Leu Thr Ile Ser Asp Asn His
690 695 700

Gln Glu Pro Gln Ser Pro Thr Ser Phe Ser Val Val Lys Gln Ser Leu
705 710 715 720

Lys Asn Ala Gln Glu Ala Glu Ala Val Val Gln Phe Lys Gly Asn Lys
725 730 735

Asp Ala Asp Phe Tyr Glu Val Tyr Glu Lys Asp Gly Asp Ser Trp Lys
740 745 750

Leu Leu Thr Gly Ser Ser Ser Thr Thr Ile Tyr Leu Pro Lys Val Ser
755 760 765

Arg Ser Ala Ser Ala Gln Gly Thr Thr Gln Glu Leu Lys Val Val Ala
770 775 780

Val Gly Lys Asn Gly Val Arg Ser Glu Ala Ala Thr Thr Thr Phe Asp
785 790 795 800

Trp Gly Met Thr Val Lys Asp Thr Ser Leu Pro Lys Pro Leu Ala Glu
805 810 815

Asn Ile Val Pro Gly Ala Thr Val Ile Asp Ser Thr Phe Pro Lys Thr
820 825 830

Glu Gly Gly Glu Gly Ile Glu Gly Met Leu Asn Gly Thr Ile Thr Ser
835 840 845

Leu Ser Asp Lys Trp Ser Ser Ala Gln Leu Ser Gly Ser Val Asp Ile
850 855 860

Arg Leu Thr Lys Pro Arg Thr Val Val Arg Trp Val Met Asp His Ala
865 870 875 880

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Gly Ala Gly Gly Glu Ser Val Asn Asp Gly Leu Met Asn Thr Lys Asp
                885                 890                 895

Phe Asp Leu Tyr Tyr Lys Asp Ala Asp Gly Glu Trp Lys Leu Ala Lys
            900                 905                 910

Glu Val Arg Gly Asn Lys Ala His Val Thr Asp Ile Thr Leu Asp Lys
        915                 920                 925

Pro Ile Thr Ala Gln Asp Trp Arg Leu Asn Val Val Thr Ser Asp Asn
    930                 935                 940

Gly Thr Pro Trp Lys Ala Ile Arg Ile Tyr Asn Trp Lys Met Tyr Glu
945                 950                 955                 960

Lys Leu Asp Thr Glu Ser Val Asn Ile Pro Met Ala Lys Ala Ala Ala
                965                 970                 975

Arg Ser Leu Gly Asn Asn Lys Val Gln Val Gly Phe Ala Asp Val Pro
            980                 985                 990

Ala Gly Ala Thr Ile Thr Val Tyr  Asp Asn Pro Asn Ser  Gln Thr Pro
        995                 1000                1005

Leu Ala  Thr Leu Lys Ser Glu  Val Gly Gly Asp Leu  Ala Ser Ala
    1010                1015                1020

Pro Leu  Asp Leu Thr Asn Gln  Ser Gly Leu Leu Tyr  Tyr Arg Thr
    1025                1030                1035

Gln Leu  Pro Gly Lys Glu Ile  Ser Asn Val Leu Ala  Val Ser Val
    1040                1045                1050

Pro Lys  Asp Asp Arg Arg Ile  Lys Ser Val Ser Leu  Glu Thr Gly
    1055                1060                1065

Pro Lys  Lys Thr Ser Tyr Ala  Glu Gly Glu Asp Leu  Asp Leu Arg
    1070                1075                1080

Gly Gly  Val Leu Arg Val Gln  Tyr Glu Gly Gly Thr  Glu Asp Glu
    1085                1090                1095

Leu Ile  Arg Leu Thr His Ala  Gly Val Ser Val Ser  Gly Phe Asp
    1100                1105                1110

Thr His  His Lys Gly Glu Gln  Asn Leu Thr Leu Gln  Tyr Leu Gly
    1115                1120                1125

Gln Pro  Val Asn Ala Asn Leu  Ser Val Thr Val Thr  Gly Gln Asp
    1130                1135                1140
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Glu Ala Ser Pro Lys Thr Ile Leu Gly Ile Glu Val Ser Gln Glu
1145 1150 1155

Pro Lys Lys Asp Tyr Leu Val Gly Asp Ser Leu Asp Leu Ser Glu
1160 1165 1170

Gly Arg Phe Ala Val Ala Tyr Ser Asn Asp Thr Met Glu Glu His
1175 1180 1185

Ser Phe Thr Asp Glu Gly Val Glu Ile Ser Gly Tyr Asp Ala Gln
1190 1195 1200

Lys Thr Gly Arg Gln Thr Leu Thr Leu His Tyr Gln Gly His Glu
1205 1210 1215

Val Ser Phe Asp Val Leu Val Ser Pro Lys Ala Ala Leu Asn Asp
1220 1225 1230

Glu Tyr Leu Lys Gln Lys Leu Ala Glu Val Glu Ala Ala Lys Asn
1235 1240 1245

Lys Val Val Tyr Asn Phe Ala Ser Ser Glu Val Lys Glu Ala Phe
1250 1255 1260

Leu Lys Ala Ile Glu Ala Ala Glu Gln Val Leu Lys Asp His Glu
1265 1270 1275

Thr Ser Thr Gln Asp Gln Val Asn Asp Arg Leu Asn Lys Leu Thr
1280 1285 1290

Glu Ala His Lys Ala Leu Asn Gly Gln Glu Lys Phe Thr Glu Glu
1295 1300 1305

Lys Thr Glu Leu Asp Arg Leu Thr Gly Glu Val Gln Glu Leu Leu
1310 1315 1320

Ala Ala Lys Pro Asn His Pro Ser Gly Ser Ala Leu Ala Pro Leu
1325 1330 1335

Leu Glu Lys Asn Lys Ala Leu Val Glu Lys Val Asp Leu Ser Pro
1340 1345 1350

Glu Glu Leu Thr Thr Ala Lys Gln Ser Leu Lys Asp Leu Val Ala
1355 1360 1365

Leu Leu Lys Glu Asp Lys Pro Ala Val Phe Ser Asp Ser Lys Thr
1370 1375 1380

Gly Val Glu Val His Phe Ser Asn Lys Glu Lys Thr Val Ile Lys
1385 1390 1395

Gly Leu Lys Val Glu Arg Val Gln Ala Ser Ala Glu Glu Lys Lys
1400 1405 1410

Tyr Phe Ala Gly Glu Asp Ala His Val Phe Glu Ile Glu Gly Leu
1415 1420 1425

Asp Glu Lys Gly Gln Asp Val Asp Leu Ser Tyr Ala Ser Ile Val
1430 1435 1440

Lys Ile Pro Ile Glu Lys Asp Lys Lys Val Lys Lys Val Phe Phe
1445 1450 1455

Leu Pro Glu Gly Lys Glu Ala Val Glu Leu Ala Phe Glu Gln Thr
1460 1465 1470

Asp Ser His Val Ile Phe Thr Ala Pro His Phe Thr His Tyr Ala
1475 1480 1485

Phe Val Tyr Glu Ser Ala Glu Lys Pro Gln Pro Ala Lys Pro Ala
1490 1495 1500

Pro Gln Asn Thr Val Leu Pro Lys Pro Thr Tyr Gln Pro Thr Ser
1505 1510 1515

Asp Gln Gln Lys Ala Pro Lys Leu Glu Val Gln Glu Glu Lys Val
1520 1525 1530

Ala Phe His Arg Gln Glu His Glu Asn Thr Glu Met Leu Val Gly
1535 1540 1545

Glu Gln Arg Val Ile Ile Gln Gly Arg Asp Gly Leu Leu Arg His
1550 1555 1560

Val Phe Glu Val Asp Glu Asn Gly Gln Arg Arg Leu Arg Ser Thr
1565 1570 1575

Glu Val Ile Gln Glu Ala Ile Pro Glu Ile Val Glu Ile Gly Thr
1580 1585 1590

Lys Val Lys Thr Val Pro Ala Val Val Ala Thr Gln Glu Lys Pro
1595 1600 1605

Ala Gln Asn Thr Ala Val Lys Ser Glu Glu Ala Ser Lys Gln Leu
1610 1615 1620

Pro Asn Thr Gly Thr Ala Asp Ala Asn Glu Ala Leu Ile Ala Gly
1625 1630 1635

Leu Ala Ser Leu Gly Leu Ala Ser Leu Ala Leu Thr Leu Arg Arg
1640 1645 1650

Lys Arg Glu Asp Lys Asp
1655

<210> 171

<211> 487

<212> PRT

<213> Streptococcus pneumoniae

<400> 171

Met Ser Ile Thr Ser Phe Val Lys Arg Ile Gln Asp Ile Thr Arg Asn
1 5 10 15

Asp Ala Gly Val Asn Gly Asp Ala Gln Arg Ile Glu Gln Met Ser Trp
20 25 30

Leu Leu Phe Leu Lys Ile Tyr Asp Ser Arg Glu Met Val Trp Glu Leu
35 40 45

Glu Glu Asp Glu Tyr Glu Ser Ile Ile Pro Glu Glu Leu Lys Trp Arg
50 55 60

Asn Trp Ala His Ala Gln Asn Gly Glu Arg Val Leu Thr Gly Asp Glu
65 70 75 80

Leu Leu Asp Phe Val Asn Asn Lys Leu Phe Lys Glu Leu Lys Glu Leu
85 90 95

Glu Ile Thr Ser Asn Met Pro Ile Arg Lys Thr Ile Val Lys Ser Ala
100 105 110

Phe Glu Asp Ala Asn Asn Tyr Met Lys Asn Gly Val Leu Leu Arg Gln
115 120 125

Val Ile Asn Val Ile Asp Glu Val Asp Phe Asn Ser Pro Glu Asp Arg
130 135 140

His Ser Phe Asn Asp Ile Tyr Glu Lys Ile Leu Lys Asp Ile Gln Asn
145 150 155 160

Ala Gly Asn Ser Gly Glu Phe Tyr Thr Pro Arg Ala Ala Thr Asp Phe
165 170 175

Ile Ala Glu Val Leu Asp Pro Lys Leu Gly Glu Ser Met Ala Asp Leu
180 185 190

Ala Cys Gly Thr Gly Gly Phe Leu Thr Ser Thr Leu Asn Arg Leu Ser
195 200 205

Ser Gln Arg Lys Thr Ser Glu Asp Thr Lys Lys Tyr Asn Thr Ala Val
210 215 220

Phe Gly Ile Glu Lys Lys Ala Phe Pro His Leu Leu Ala Val Thr Asn
225 230 235 240

Leu Phe Leu His Glu Ile Asp Asp Pro Lys Ile Val His Gly Asn Thr
245 250 255

Leu Glu Lys Asn Val Arg Glu Tyr Thr Asp Asp Glu Lys Phe Asp Ile
260 265 270

Ile Met Met Asn Pro Pro Phe Gly Gly Ser Glu Leu Glu Thr Ile Lys
275 280 285

Asn Asn Phe Pro Ala Glu Leu Arg Ser Ser Glu Thr Ala Asp Leu Phe
290 295 300

Met Ala Val Ile Met Tyr Arg Leu Lys Glu Asn Gly Arg Val Gly Val
305 310 315 320

Ile Leu Pro Asp Gly Phe Leu Phe Gly Glu Gly Val Lys Thr Arg Leu
325 330 335

Lys Gln Lys Leu Val Asp Glu Phe Asn Leu His Thr Ile Ile Arg Leu
340 345 350

Pro His Ser Val Phe Ala Pro Tyr Thr Gly Ile His Thr Asn Ile Leu
355 360 365

Phe Phe Asp Lys Thr Lys Lys Thr Glu Glu Thr Trp Phe Tyr Arg Leu
370 375 380

Asp Met Pro Asp Gly Tyr Lys Asn Phe Ser Lys Thr Lys Pro Met Lys
385 390 395 400

Ser Glu His Phe Asn Pro Val Arg Asp Trp Trp Glu Asn Arg Glu Glu
405 410 415

Ile Leu Glu Gly Lys Phe Tyr Lys Ser Lys Ser Phe Thr Pro Ser Glu
420 425 430

Leu Ala Glu Leu Asn Tyr Asn Leu Asp Gln Cys Asp Phe Pro Lys Glu
435 440 445

Glu Glu Glu Ile Leu Asn Pro Phe Glu Leu Ile Gln Asn Tyr Gln Ala
450 455 460

Glu Arg Ala Thr Leu Asn His Lys Ile Asp Asn Val Leu Ala Asp Ile
465 470 475 480

Leu Gln Leu Leu Glu Asp Lys
485

<210> 172

<211> 378

<212> PRT

<213> Streptococcus pneumoniae

<400> 172

Met Asn Asn Thr Glu Phe Tyr Asp Arg Leu Gly Val Ser Lys Asn Ala
1 5 10 15

Ser Ala Asp Glu Ile Lys Lys Ala Tyr Arg Lys Leu Ser Lys Lys Tyr
20 25 30

His Pro Asp Ile Asn Lys Glu Pro Gly Ala Glu Asp Lys Tyr Lys Glu
35 40 45

Val Gln Glu Ala Tyr Glu Thr Leu Ser Asp Asp Gln Lys Arg Ala Ala
50 55 60

Tyr Asp Gln Tyr Gly Ala Ala Gly Ala Asn Gly Gly Phe Gly Gly Ala
65 70 75 80

Gly Gly Phe Gly Gly Phe Asn Gly Ala Gly Gly Phe Gly Gly Phe Glu
85 90 95

Asp Ile Phe Ser Ser Phe Phe Gly Gly Gly Gly Ser Ser Arg Asn Pro
100 105 110

Asn Ala Pro Arg Gln Gly Asp Asp Leu Gln Tyr Arg Val Asn Leu Thr
115 120 125

Phe Glu Glu Ala Ile Phe Gly Thr Glu Lys Glu Val Lys Tyr His Arg
130 135 140

Glu Ala Gly Cys Arg Thr Cys Asn Gly Ser Gly Ala Lys Pro Gly Thr
145 150 155 160

Ser Pro Val Thr Cys Gly Arg Cys His Gly Ala Gly Val Ile Asn Val
165 170 175

Asp Thr Gln Thr Pro Leu Gly Met Met Arg Arg Gln Val Thr Cys Asp
180 185 190

Val Cys His Gly Arg Gly Lys Glu Ile Lys Tyr Pro Cys Thr Thr Cys
195 200 205

His Gly Thr Gly His Glu Lys Gln Ala His Ser Val His Val Lys Ile
210 215 220

Pro Ala Gly Val Glu Thr Gly Gln Gln Ile Arg Leu Ala Gly Gln Gly
225 230 235 240

Glu Ala Gly Phe Asn Gly Gly Pro Tyr Gly Asp Leu Tyr Val Val Val
245 250 255

Ser Val Glu Ala Ser Asp Lys Phe Glu Arg Glu Gly Thr Thr Ile Phe
260 265 270

Tyr Asn Leu Asn Leu Asn Phe Val Gln Ala Ala Leu Gly Asp Thr Val
275 280 285

Asp Ile Pro Thr Val His Gly Asp Val Glu Leu Val Ile Pro Glu Gly
290 295 300

Thr Gln Thr Gly Lys Lys Phe Arg Leu Arg Ser Lys Gly Ala Pro Ser
305 310 315 320

Leu Arg Gly Gly Ala Val Gly Asp Gln Tyr Val Thr Val Asn Val Val
325 330 335

Thr Pro Thr Gly Leu Asn Asp Arg Gln Lys Val Ala Leu Lys Glu Phe
340 345 350

Ala Ala Ala Gly Asp Leu Lys Val Asn Pro Lys Lys Lys Gly Phe Phe
355 360 365

Asp His Ile Lys Asp Ala Phe Asp Gly Glu
370 375

<210> 173

<211> 453

<212> PRT

<213> Streptococcus pneumoniae

<400> 173

Met Asn Pro Asn Leu Phe Arg Ser Val Glu Phe Tyr Gln Arg Arg Tyr
1 5 10 15

His Asn Tyr Ala Thr Val Leu Ile Ile Pro Leu Ser Leu Leu Phe Thr
20 25 30

Phe Ile Leu Ile Phe Ser Leu Val Ala Thr Lys Glu Ile Thr Val Thr
35 40 45

Ser Gln Gly Glu Ile Ala Pro Thr Ser Val Ile Ala Ser Ile Gln Ser
50 55 60

Thr Ser Asp Asn Pro Ile Leu Ala Asn His Leu Val Ala Asn Gln Val
65 70 75 80

Val Glu Lys Gly Asp Leu Leu Ile Lys Tyr Ser Glu Thr Met Glu Glu
85 90 95

Ser Gln Lys Thr Ala Leu Ala Thr Gln Leu Gln Arg Leu Glu Lys Gln
100 105 110

Lys Glu Gly Leu Gly Ile Leu Lys Gln Ser Leu Glu Lys Ala Thr Asp
115 120 125

Leu Phe Ser Gly Glu Asp Glu Phe Gly Tyr His Asn Thr Phe Met Asn
130 135 140

Phe Thr Lys Gln Ser His Asp Ile Glu Leu Gly Ile Thr Lys Thr Asn
145 150 155 160

Thr Glu Val Ser Asn Gln Ala Asn Leu Ser Asn Ser Ser Ser Ser Ala
165 170 175

Ile Glu Gln Glu Ile Thr Lys Val Gln Gln Gln Ile Gly Glu Tyr Gln
180 185 190

Glu Leu Arg Asp Ala Ile Ile Asn Asn Arg Ala Arg Leu Pro Thr Gly
195 200 205

Asn Pro His Gln Ser Ile Leu Asn Arg Tyr Leu Val Ala Ser Gln Gly
210 215 220

Gln Thr Gln Gly Thr Ala Glu Glu Pro Phe Leu Ser Gln Ile Asn Gln
225 230 235 240

Ser Ile Ala Gly Leu Glu Ser Ser Ile Ala Ser Leu Lys Ile Gln Gln
245 250 255

Ala Gly Ile Gly Ser Val Ala Thr Tyr Asp Asn Ser Leu Ala Thr Lys
260 265 270

Ile Glu Val Leu Arg Thr Gln Phe Leu Gln Thr Ala Ser Gln Gln Gln
275 280 285

Leu Thr Val Glu Asn Gln Leu Thr Glu Leu Lys Val Gln Leu Asp Gln
290 295 300

Ala Thr Gln Arg Leu Glu Asn Asn Thr Leu Thr Ser Pro Ser Lys Gly
305 310 315 320

Ile Val His Leu Asn Ser Glu Phe Glu Gly Lys Asn Arg Ile Pro Thr
325 330 335

Gly Thr Glu Ile Ala Gln Ile Phe Pro Val Ile Thr Asp Thr Arg Glu
340 345 350

Val Leu Ile Thr Tyr Tyr Val Ser Ser Asp Tyr Leu Pro Leu Leu Asp
355 360 365

Lys Gly Gln Thr Val Arg Leu Lys Leu Glu Lys Ile Gly Asn His Gly
370 375 380

Thr Thr Ile Ile Gly Gln Leu Gln Thr Ile Asp Gln Thr Pro Thr Arg
385 390 395 400

Thr Glu Gln Gly Asn Leu Phe Lys Leu Thr Ala Leu Ala Lys Leu Ser
405 410 415

Asn Glu Asp Ser Lys Leu Ile Gln Tyr Gly Leu Gln Gly Arg Val Thr
420 425 430

Ser Val Thr Thr Lys Lys Thr Tyr Phe Asp Tyr Phe Lys Asp Lys Ile
435 440 445

Leu Thr His Ser Asp
450

<210> 174

<211> 131

<212> PRT

<213> Streptococcus pneumoniae

<400> 174

Met Ser Lys Lys Leu Asn Arg Lys Lys Gln Leu Arg Asn Gly Leu Arg
1 5 10 15

Arg Ala Gly Ala Phe Ser Ser Thr Val Thr Lys Val Val Asp Glu Thr
20 25 30

Lys Lys Val Val Lys Arg Ala Glu Gln Ser Ala Ser Ala Ala Gly Lys
35 40 45

Ala Val Ser Lys Lys Val Glu Gln Ala Val Glu Ala Thr Lys Glu Gln
50 55 60

Ala Gln Lys Val Ala Asn Ser Val Glu Asp Phe Ala Ala Asn Leu Gly
65 70 75 80

Gly Leu Pro Leu Asp Arg Ala Lys Thr Phe Tyr Asp Glu Gly Ile Lys
85 90 95

Ser Ala Ser Asp Phe Lys Asn Trp Thr Glu Lys Glu Leu Leu Ala Leu
100 105 110

Lys Gly Ile Gly Pro Ala Thr Ile Lys Lys Leu Lys Glu Asn Gly Ile
115 120 125

Lys Phe Lys
130

<210> 175

<211> 254

<212> PRT

<213> Streptococcus pneumoniae

<400> 175

Leu Ile Ser Leu Phe Gly Leu Ala Ala Ala Lys Pro Val Gln Ala Asp
1 5 10 15

Thr Ser Ile Ala Asp Ile Gln Lys Arg Gly Glu Leu Val Val Gly Val
20 25 30

Lys Gln Asp Val Pro Asn Phe Gly Tyr Lys Asp Pro Lys Thr Gly Thr
35 40 45

Tyr Ser Gly Ile Glu Thr Asp Leu Ala Lys Met Val Ala Asp Glu Leu
50 55 60

Lys Val Lys Ile Arg Tyr Val Pro Val Thr Ala Gln Thr Arg Gly Pro
65 70 75 80

Leu Leu Asp Asn Glu Gln Val Asp Met Asp Ile Ala Thr Phe Thr Ile
85 90 95

Thr Asp Glu Arg Lys Lys Leu Tyr Asn Phe Thr Ser Pro Tyr Tyr Thr
100 105 110

Asp Ala Ser Gly Phe Leu Val Asn Lys Ser Ala Lys Ile Lys Lys Ile
115 120 125

Glu Asp Leu Asn Gly Lys Thr Ile Gly Val Ala Gln Gly Ser Ile Thr
130 135 140

Gln Arg Leu Ile Thr Glu Leu Gly Lys Lys Lys Gly Leu Lys Phe Lys
145 150 155 160

Phe Val Glu Leu Gly Ser Tyr Pro Glu Leu Ile Thr Ser Leu His Ala
165 170 175

His Arg Ile Asp Thr Phe Ser Val Asp Arg Ser Ile Leu Ser Gly Tyr
180 185 190

Thr Ser Lys Arg Thr Ala Leu Leu Asp Asp Ser Phe Lys Pro Ser Asp
195 200 205

Tyr Gly Ile Val Thr Lys Lys Ser Asn Thr Glu Leu Asn Asp Tyr Leu
210 215 220

Asp Asn Leu Val Thr Lys Trp Ser Lys Asp Gly Ser Leu Gln Lys Leu
225 230 235 240

Tyr Asp Arg Tyr Lys Leu Lys Pro Ser Ser His Thr Ala Asp
245 250

<210> 176

<211> 553

<212> PRT

<213> Streptococcus pneumoniae

<400> 176

Met Ser Asn Ile Ser Leu Thr Thr Leu Gly Gly Val Arg Glu Asn Gly
1 5 10 15

Lys Asn Met Tyr Ile Ala Glu Ile Gly Glu Ser Ile Phe Val Leu Asn
20 25 30

Val Gly Leu Lys Tyr Pro Glu Asn Glu Gln Leu Gly Val Asp Val Val
35 40 45

Ile Pro Asn Met Asp Tyr Leu Phe Glu Asn Ser Asp Arg Ile Ala Gly
50 55 60

Val Phe Leu Thr His Gly His Ala Asp Ala Ile Gly Ala Leu Pro Tyr
65 70 75 80

Leu Leu Ala Glu Ala Lys Val Pro Val Phe Gly Ser Glu Leu Thr Ile
85 90 95

Glu Leu Ala Lys Leu Phe Val Lys Gly Asn Asp Ala Val Lys Lys Phe
100 105 110

Asn Asp Phe His Val Ile Asp Glu Asn Thr Glu Ile Asp Phe Gly Gly
115 120 125

Thr Val Val Ser Phe Phe Pro Thr Thr Tyr Ser Val Pro Glu Ser Leu
130 135 140

Gly Ile Val Leu Lys Thr Ser Glu Gly Ser Ile Val Tyr Thr Gly Asp
145 150 155 160

Phe Lys Phe Asp Gln Thr Ala Ser Glu Ser Tyr Ala Thr Asp Phe Ala
165 170 175

Arg Leu Ala Glu Ile Gly Arg Asp Gly Val Leu Ala Leu Leu Ser Asp
180 185 190

Ser Ala Asn Ala Asp Ser Asn Ile Gln Val Ala Ser Glu Ser Glu Val
195 200 205

Arg Asp Glu Ile Thr Gln Thr Ile Ala Asp Trp Glu Gly Arg Ile Ile
210 215 220

Val Ala Ala Val Ser Ser Asn Leu Ser Arg Ile Gln Gln Ile Phe Asp
225 230 235 240

Ala Ala Asp Lys Thr Gly Arg Arg Ile Val Leu Thr Gly Phe Asp Ile
245 250 255

Glu Asn Ile Val Arg Thr Ala Ile Arg Leu Lys Lys Leu Ser Leu Ala
260 265 270

Asn Glu Ile Leu Leu Ile Lys Pro Lys Asp Met Ser Arg Phe Glu Asp
275 280 285

His Glu Leu Ile Ile Leu Glu Thr Gly Arg Met Gly Glu Pro Ile Asn
290 295 300

Gly Leu Arg Lys Met Ser Ile Gly Arg His Arg Tyr Val Glu Ile Lys
305 310 315 320

Asp Gly Asp Leu Val Tyr Ile Ala Thr Ala Pro Ser Ile Ala Lys Glu
325 330 335

Ala Phe Val Ala Arg Val Glu Asn Met Ile Tyr Gln Ala Gly Gly Val
340 345 350

Val Lys Leu Ile Thr Gln Ser Leu His Val Ser Gly His Gly Asn Val
355 360 365

Arg Asp Leu Gln Leu Met Ile Asn Leu Leu Gln Pro Lys Tyr Leu Phe
370 375 380

Pro Val Gln Gly Glu Tyr Arg Glu Leu Asp Ala His Ala Lys Ala Ala
385 390 395 400

Met Ala Val Gly Met Leu Pro Glu Arg Ile Phe Ile Pro Lys Lys Gly
405 410 415

Thr Thr Met Ala Tyr Glu Asn Gly Asp Phe Val Pro Ala Gly Ser Val
420 425 430

Ser Ala Gly Asp Ile Leu Ile Asp Gly Asn Ala Ile Gly Asp Val Gly
435 440 445

Asn Val Val Leu Arg Asp Arg Lys Val Leu Ser Glu Asp Gly Ile Phe
450 455 460

Ile Val Ala Ile Thr Val Asn Arg Arg Glu Lys Lys Ile Val Ala Arg
465 470 475 480

Ala Arg Val His Thr Arg Gly Phe Val Tyr Leu Lys Lys Ser Arg Asp
485 490 495

Ile Leu Arg Glu Ser Ser Glu Leu Ile Asn Gln Thr Val Glu Glu Tyr
500 505 510

Leu Gln Gly Asp Asp Phe Asp Trp Ala Asp Leu Lys Gly Lys Val Arg
515 520 525

Asp Asn Leu Thr Lys Tyr Leu Phe Asp Gln Thr Lys Arg Arg Pro Ala
530 535 540

Ile Leu Pro Val Val Met Glu Ala Lys
545 550

<210> 177

<211> 2140

<212> PRT

<213> Streptococcus pneumoniae

<400> 177

Met Lys Lys Ser Thr Val Leu Ser Leu Thr Thr Ala Ala Val Ile Leu
1 5 10 15

Ala Ala Tyr Ala Pro Asn Glu Val Val Leu Ala Asp Thr Ser Ser Ser
20 25 30

Glu Asp Ala Leu Asn Ile Ser Asp Lys Glu Lys Val Ala Glu Asn Lys
35 40 45

Glu Lys His Glu Asn Ile His Ser Ala Met Glu Thr Ser Gln Asp Phe
50 55 60

Lys Glu Lys Lys Thr Ala Val Ile Lys Glu Lys Glu Val Val Ser Lys
65 70 75 80

Asn Pro Val Ile Asp Asn Asn Thr Ser Asn Glu Glu Ala Lys Ile Lys
85 90 95

Glu Glu Asn Ser Asn Lys Ser Gln Gly Asp Tyr Thr Asp Ser Phe Val
100 105 110

Asn Lys Asn Thr Glu Asn Pro Lys Lys Glu Asp Lys Val Val Tyr Ile
115 120 125

Ala Glu Phe Lys Asp Lys Glu Ser Gly Glu Lys Ala Ile Lys Glu Leu
130 135 140

Ser Ser Leu Lys Asn Thr Lys Val Leu Tyr Thr Tyr Asp Arg Ile Phe
145 150 155 160

Asn Gly Ser Ala Ile Glu Thr Thr Pro Asp Asn Leu Asp Lys Ile Lys
165 170 175

Gln Ile Glu Gly Ile Ser Ser Val Glu Arg Ala Gln Lys Val Gln Pro
180 185 190

Met Met Asn His Ala Arg Lys Glu Ile Gly Val Glu Glu Ala Ile Asp
195 200 205

Tyr Leu Lys Ser Ile Asn Ala Pro Phe Gly Lys Asn Phe Asp Gly Arg
210 215 220

Gly Met Val Ile Ser Asn Ile Asp Thr Gly Thr Asp Tyr Arg His Lys
225 230 235 240

Ala Met Arg Ile Asp Asp Asp Ala Lys Ala Ser Met Arg Phe Lys Lys
245 250 255

Glu Asp Leu Lys Gly Thr Asp Lys Asn Tyr Trp Leu Ser Asp Lys Ile
260 265 270

Pro His Ala Phe Asn Tyr Tyr Asn Gly Gly Lys Ile Thr Val Glu Lys
275 280 285

Tyr Asp Asp Gly Arg Asp Tyr Phe Asp Pro His Gly Met His Ile Ala
290 295 300

Gly Ile Leu Ala Gly Asn Asp Thr Glu Gln Asp Ile Lys Asn Phe Asn
305 310 315 320

Gly Ile Asp Gly Ile Ala Pro Asn Ala Gln Ile Phe Ser Tyr Lys Met
325 330 335

Tyr Ser Asp Ala Gly Ser Gly Phe Ala Gly Asp Glu Thr Met Phe His
340 345 350

Ala Ile Glu Asp Ser Ile Lys His Asn Val Asp Val Val Ser Val Ser
355 360 365

Ser Gly Phe Thr Gly Thr Gly Leu Val Gly Glu Lys Tyr Trp Gln Ala
370 375 380

Ile Arg Ala Leu Arg Lys Ala Gly Ile Pro Met Val Val Ala Thr Gly
385 390 395 400

Asn Tyr Ala Thr Ser Ala Ser Ser Ser Ser Trp Asp Leu Val Ala Asn
405 410 415

Asn His Leu Lys Met Thr Asp Thr Gly Asn Val Thr Arg Thr Ala Ala
420 425 430

His Glu Asp Ala Ile Ala Val Ala Ser Ala Lys Asn Gln Thr Val Glu
435 440 445

Phe Asp Lys Val Asn Ile Gly Gly Glu Ser Phe Lys Tyr Arg Asn Ile
450 455 460

Gly Ala Phe Phe Asp Lys Ser Lys Ile Thr Thr Asn Glu Asp Gly Thr
465 470 475 480

Lys Ala Pro Ser Lys Leu Lys Phe Val Tyr Ile Gly Lys Gly Gln Asp
485 490 495

Gln Asp Leu Ile Gly Leu Asp Leu Arg Gly Lys Ile Ala Val Met Asp
500 505 510

Arg Ile Tyr Thr Lys Asp Leu Lys Asn Ala Phe Lys Lys Ala Met Asp
515 520 525

Lys Gly Ala Arg Ala Ile Met Val Val Asn Thr Val Asn Tyr Tyr Asn
530 535 540

Arg Asp Asn Trp Thr Glu Leu Pro Ala Met Gly Tyr Glu Ala Asp Glu
545 550 555 560

Gly Thr Lys Ser Gln Val Phe Ser Ile Ser Gly Asp Asp Gly Val Lys
565 570 575

Leu Trp Asn Met Ile Asn Pro Asp Lys Lys Thr Glu Val Lys Arg Asn
580 585 590

Asn Lys Glu Asp Phe Lys Asp Lys Leu Glu Gln Tyr Tyr Pro Ile Asp
595 600 605

Met Glu Ser Phe Asn Ser Asn Lys Pro Asn Val Gly Asp Glu Lys Glu
610 615 620

Ile Asp Phe Lys Phe Ala Pro Asp Thr Asp Lys Glu Leu Tyr Lys Glu
625 630 635 640

Asp Ile Ile Val Pro Ala Gly Ser Thr Ser Trp Gly Pro Arg Ile Asp
645 650 655

Leu Leu Leu Lys Pro Asp Val Ser Ala Pro Gly Lys Asn Ile Lys Ser
660 665 670

Thr Leu Asn Val Ile Asn Gly Lys Ser Thr Tyr Gly Tyr Met Ser Gly
675 680 685

Thr Ser Met Ala Thr Pro Ile Val Ala Ala Ser Thr Val Leu Ile Arg
690 695 700

Pro Lys Leu Lys Glu Met Leu Glu Arg Pro Val Leu Lys Asn Leu Lys
705 710 715 720

Gly Asp Asp Lys Ile Asp Leu Thr Ser Leu Thr Lys Ile Ala Leu Gln
725 730 735

Asn Thr Ala Arg Pro Met Met Asp Ala Thr Ser Trp Lys Glu Lys Ser
740 745 750

Gln Tyr Phe Ala Ser Pro Arg Gln Gln Gly Ala Gly Leu Ile Asn Val
755 760 765

Ala Asn Ala Leu Arg Asn Glu Val Val Ala Thr Phe Lys Asn Thr Asp
770 775 780

Ser Lys Gly Leu Val Asn Ser Tyr Gly Ser Ile Ser Leu Lys Glu Ile
785 790 795 800

Lys Gly Asp Lys Lys Tyr Phe Thr Ile Lys Leu His Asn Thr Ser Asn
805 810 815

Arg Pro Leu Thr Phe Lys Val Ser Ala Ser Ala Ile Thr Thr Asp Ser
820 825 830

Leu Thr Asp Arg Leu Lys Leu Asp Glu Thr Tyr Lys Asp Glu Lys Ser
835 840 845

Pro Asp Gly Lys Gln Ile Val Pro Glu Ile His Pro Glu Lys Val Lys
850 855 860

Gly Ala Asn Ile Thr Phe Glu His Asp Thr Phe Thr Ile Gly Ala Asn
865 870 875 880

Ser Ser Phe Asp Leu Asn Ala Val Ile Asn Val Gly Glu Ala Lys Asn
885 890 895

Lys Asn Lys Phe Val Glu Ser Phe Ile His Phe Glu Ser Val Glu Glu
900 905 910

Met Glu Ala Leu Asn Ser Asn Gly Lys Lys Ile Asn Phe Gln Pro Ser
915 920 925

Leu Ser Met Pro Leu Met Gly Phe Ala Gly Asn Trp Asn His Glu Pro
930 935 940

Ile Leu Asp Lys Trp Ala Trp Glu Glu Gly Ser Arg Ser Lys Thr Leu
945 950 955 960

Gly Gly Tyr Asp Asp Asp Gly Lys Pro Lys Ile Pro Gly Thr Leu Asn
965 970 975

Lys Gly Ile Gly Gly Glu His Gly Ile Asp Lys Phe Asn Pro Ala Gly
980 985 990

Val Ile Gln Asn Arg Lys Asp Lys Asn Thr Thr Ser Leu Asp Gln Asn
995 1000 1005

Pro Glu Leu Phe Ala Phe Asn Asn Glu Gly Ile Asn Ala Pro Ser
1010 1015 1020

Ser Ser Gly Ser Lys Ile Ala Asn Ile Tyr Pro Leu Asp Ser Asn
1025 1030 1035

Gly Asn Pro Gln Asp Ala Gln Leu Glu Arg Gly Leu Thr Pro Ser
1040 1045 1050

Pro Leu Val Leu Arg Ser Ala Glu Glu Gly Leu Ile Ser Ile Val
1055 1060 1065

Asn Thr Asn Lys Glu Gly Glu Asn Gln Arg Asp Leu Lys Val Ile
1070 1075 1080

Ser Arg Glu His Phe Ile Arg Gly Ile Leu Asn Ser Lys Ser Asn
1085 1090 1095

Asp Ala Lys Gly Ile Lys Ser Ser Lys Leu Lys Val Trp Gly Asp
1100 1105 1110

Leu Lys Trp Asp Gly Leu Ile Tyr Asn Pro Arg Gly Arg Glu Glu
1115 1120 1125

Asn Ala Pro Glu Ser Lys Asp Asn Gln Asp Pro Ala Thr Lys Ile
1130 1135 1140

Arg Gly Gln Phe Glu Pro Ile Ala Glu Gly Gln Tyr Phe Tyr Lys
1145 1150 1155

Phe Lys Tyr Arg Leu Thr Lys Asp Tyr Pro Trp Gln Val Ser Tyr
1160 1165 1170

Ile Pro Val Lys Ile Asp Asn Thr Ala Pro Lys Ile Val Ser Val
1175 1180 1185

Asp Phe Ser Asn Pro Glu Lys Ile Lys Leu Ile Thr Lys Asp Thr
1190 1195 1200

Tyr His Lys Val Lys Asp Gln Tyr Lys Asn Glu Thr Leu Phe Ala
1205 1210 1215

Arg Asp Gln Lys Glu His Pro Glu Lys Phe Asp Glu Ile Ala Asn
1220 1225 1230

Glu Val Trp Tyr Ala Gly Ala Ala Leu Val Asn Glu Asp Gly Glu
1235 1240 1245

Val Glu Lys Asn Leu Glu Val Thr Tyr Ala Gly Glu Gly Gln Gly
1250 1255 1260

Arg Asn Arg Lys Leu Asp Lys Asp Gly Asn Thr Ile Tyr Glu Ile
1265 1270 1275

Lys Gly Ala Gly Asp Leu Arg Gly Lys Ile Ile Glu Val Ile Ala
1280 1285 1290

Leu Asp Gly Ser Ser Asn Phe Thr Lys Ile His Arg Ile Lys Phe
1295 1300 1305

Ala Asn Gln Ala Asp Glu Lys Gly Met Ile Ser Tyr Tyr Leu Val
1310 1315 1320

Asp Pro Asp Gln Asp Ser Ser Lys Tyr Gln Lys Leu Gly Glu Ile
1325 1330 1335

Ala Glu Ser Lys Phe Lys Asn Leu Gly Asn Gly Lys Glu Gly Ser
1340 1345 1350

Leu Lys Lys Asp Thr Thr Gly Val Glu His His His Gln Glu Asn
1355 1360 1365

Glu Glu Ser Ile Lys Glu Lys Ser Ser Phe Thr Ile Asp Arg Asn
1370 1375 1380

Ile Ser Thr Ile Arg Asp Phe Glu Asn Lys Asp Leu Lys Lys Leu
1385 1390 1395

Ile Lys Lys Lys Phe Arg Glu Val Asp Asp Phe Thr Ser Glu Thr
1400 1405 1410

Gly Lys Arg Met Glu Glu Tyr Asp Tyr Lys Tyr Asp Asp Lys Gly
1415 1420 1425

Asn Ile Ile Ala Tyr Asp Asp Gly Thr Asp Leu Glu Tyr Glu Thr
1430 1435 1440

Glu Lys Leu Asp Glu Ile Lys Ser Lys Ile Tyr Gly Val Leu Ser
1445 1450 1455

Pro Ser Lys Asp Gly His Phe Glu Ile Leu Gly Lys Ile Ser Asn
1460 1465 1470

Val Ser Lys Asn Ala Lys Val Tyr Tyr Gly Asn Asn Tyr Lys Ser
1475 1480 1485

Ile Glu Ile Lys Ala Thr Lys Tyr Asp Phe His Ser Lys Thr Met
1490 1495 1500

Thr Phe Asp Leu Tyr Ala Asn Ile Asn Asp Ile Val Asp Gly Leu
1505 1510 1515

Ala Phe Ala Gly Asp Met Arg Leu Phe Val Lys Asp Asn Asp Gln
1520 1525 1530

Lys Lys Ala Glu Ile Lys Ile Arg Met Pro Glu Lys Ile Lys Glu
1535 1540 1545

Thr Lys Ser Glu Tyr Pro Tyr Val Ser Ser Tyr Gly Asn Val Ile
1550 1555 1560

Glu Leu Gly Glu Gly Asp Leu Ser Lys Asn Lys Pro Asp Asn Leu
1565 1570 1575

Thr Lys Met Glu Ser Gly Lys Ile Tyr Ser Asp Ser Glu Lys Gln
1580 1585 1590

Gln Tyr Leu Leu Lys Asp Asn Ile Ile Leu Arg Lys Gly Tyr Ala
1595 1600 1605

Leu Lys Val Thr Thr Tyr Asn Pro Gly Lys Thr Asp Met Leu Glu
1610 1615 1620

Gly Asn Gly Val Tyr Ser Lys Glu Asp Ile Ala Lys Ile Gln Lys
1625 1630 1635

Ala Asn Pro Asn Leu Arg Ala Leu Ser Glu Thr Thr Ile Tyr Ala
1640 1645 1650

Asp Ser Arg Asn Val Glu Asp Gly Arg Ser Thr Gln Ser Val Leu
1655 1660 1665

Met Ser Ala Leu Asp Gly Phe Asn Ile Ile Arg Tyr Gln Val Phe
1670 1675 1680

Thr Phe Lys Met Asn Asp Lys Gly Glu Ala Ile Asp Lys Asp Gly
1685 1690 1695

Asn Leu Val Thr Asp Ser Ser Lys Leu Val Leu Phe Gly Lys Asp
1700 1705 1710

Asp Lys Glu Tyr Thr Gly Glu Asp Lys Phe Asn Val Glu Ala Ile
1715 1720 1725

Lys Glu Asp Gly Ser Met Leu Phe Ile Asp Thr Lys Pro Val Asn
1730 1735 1740

Leu Ser Met Asp Lys Asn Tyr Phe Asn Pro Ser Lys Ser Asn Lys
1745 1750 1755

Ile Tyr Val Arg Asn Pro Glu Phe Tyr Leu Arg Gly Lys Ile Ser
1760 1765 1770

Asp Lys Gly Gly Phe Asn Trp Glu Leu Arg Val Asn Glu Ser Val
1775 1780 1785

Val Asp Asn Tyr Leu Ile Tyr Gly Asp Leu His Ile Asp Asn Thr
1790 1795 1800

Arg Asp Phe Asn Ile Lys Leu Asn Val Lys Asp Gly Asp Ile Met
1805 1810 1815

Asp Trp Gly Met Lys Asp Tyr Lys Ala Asn Gly Phe Pro Asp Lys
1820 1825 1830

Val Thr Asp Met Asp Gly Asn Val Tyr Leu Gln Thr Gly Tyr Ser
1835 1840 1845

Asp Leu Asn Ala Lys Ala Val Gly Val His Tyr Gln Phe Leu Tyr
1850 1855 1860

Asp Asn Val Lys Pro Glu Val Asn Ile Asp Pro Lys Gly Asn Thr
1865 1870 1875

Ser Ile Glu Tyr Ala Asp Gly Lys Ser Val Val Phe Asn Ile Asn
1880 1885 1890

Asp Lys Arg Asn Asn Gly Phe Asp Gly Glu Ile Gln Glu Gln His
1895 1900 1905

Ile Tyr Ile Asn Gly Lys Glu Tyr Thr Ser Phe Asn Asp Ile Lys
1910 1915 1920

Gln Ile Ile Asp Lys Thr Leu Asn Ile Lys Ile Val Val Lys Asp
1925 1930 1935

Phe Ala Arg Asn Thr Thr Val Lys Glu Phe Ile Leu Asn Lys Asp
1940 1945 1950

Thr Gly Glu Val Ser Glu Leu Lys Pro His Arg Val Thr Val Thr
1955 1960 1965

Ile Gln Asn Gly Lys Glu Met Ser Ser Thr Ile Val Ser Glu Glu
1970 1975 1980

Asp Phe Ile Leu Pro Val Tyr Lys Gly Glu Leu Glu Lys Gly Tyr
1985 1990 1995

Gln Phe Asp Gly Trp Glu Ile Ser Gly Phe Glu Gly Lys Lys Asp
2000 2005 2010

Ala Gly Tyr Val Ile Asn Leu Ser Lys Asp Thr Phe Ile Lys Pro
2015 2020 2025

Val Phe Lys Lys Ile Glu Glu Lys Lys Glu Glu Glu Asn Lys Pro
2030 2035 2040

Thr Phe Asp Val Ser Lys Lys Lys Asp Asn Pro Gln Val Asn His
2045 2050 2055

Ser Gln Leu Asn Glu Ser His Arg Lys Glu Asp Leu Gln Arg Glu
2060 2065 2070

Glu His Ser Gln Lys Ser Asp Ser Thr Lys Asp Val Thr Ala Thr
2075 2080 2085

Val Leu Asp Lys Asn Asn Ile Ser Ser Lys Ser Thr Thr Asn Asn
2090 2095 2100

Pro Asn Lys Leu Pro Lys Thr Gly Thr Ala Ser Gly Ala Gln Thr
2105 2110 2115

Leu Leu Ala Ala Gly Ile Met Phe Ile Val Gly Ile Phe Leu Gly
2120 2125 2130

Leu Lys Lys Lys Asn Gln Asp
2135 2140

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<211> 2233

<212> PRT

<213> Streptococcus pneumoniae

<400> 178

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Phe Ala Val Gly Ala Cys Ser Val Met Ile Gly Thr Cys Ala Val Leu
20 25 30

Leu Gly Gly Asn Ile Ala Gly Glu Ser Val Val Tyr Ala Asp Glu Thr
35 40 45

Leu Ile Thr His Thr Ala Glu Lys Pro Lys Glu Glu Lys Met Ile Val
50 55 60

Glu Glu Lys Ala Asp Lys Ala Leu Glu Thr Lys Asn Ile Val Glu Arg
65 70 75 80

Thr Glu Gln Ser Glu Pro Ser Ser Thr Glu Ala Ile Ala Ser Glu Lys
85 90 95

Lys Glu Asp Glu Ala Val Thr Pro Lys Glu Glu Lys Val Ser Ala Lys
100 105 110

Pro Glu Glu Lys Ala Pro Arg Ile Glu Ser Gln Ala Ser Asn Gln Glu
115 120 125

Lys Pro Leu Lys Glu Asp Ala Lys Ala Val Thr Asn Glu Glu Val Asn
130 135 140

Gln Met Ile Glu Asp Arg Lys Val Asp Phe Asn Gln Asn Trp Tyr Phe
145 150 155 160

Lys Leu Asn Ala Asn Ser Lys Glu Ala Ile Lys Pro Asp Ala Asp Val
165 170 175

Ser Thr Trp Lys Lys Leu Asp Leu Pro Tyr Asp Trp Ser Ile Phe Asn
180 185 190

Asp Phe Asp His Glu Ser Pro Ala Gln Asn Glu Gly Gly Gln Leu Asn
195 200 205

Gly Gly Glu Ala Trp Tyr Arg Lys Thr Phe Lys Leu Asp Glu Lys Asp
210 215 220

Leu Lys Lys Asn Val Arg Leu Thr Phe Asp Gly Val Tyr Met Asp Ser
225 230 235 240

Gln Val Tyr Val Asn Gly Gln Leu Val Gly His Tyr Pro Asn Gly Tyr
245 250 255

Asn Gln Phe Ser Tyr Asp Ile Thr Lys Tyr Leu Gln Lys Asp Gly Arg
260 265 270

Glu Asn Val Ile Ala Val His Ala Val Asn Lys Gln Pro Ser Ser Arg
275 280 285

Trp Tyr Ser Gly Ser Gly Ile Tyr Arg Asp Val Thr Leu Gln Val Thr
290 295 300

Asp Lys Val His Val Glu Lys Asn Gly Thr Thr Ile Leu Thr Pro Lys
305 310 315 320

Leu Glu Glu Gln Gln His Gly Lys Val Glu Thr His Val Thr Ser Lys
325 330 335

Ile Val Asn Thr Asp Asp Lys Asp His Glu Leu Val Ala Glu Tyr Gln
340 345 350

Ile Val Glu Arg Gly Gly His Ala Val Thr Gly Leu Val Arg Thr Ala
355 360 365

Ser Arg Thr Leu Lys Ala His Glu Ser Thr Ser Leu Asp Ala Ile Leu
370 375 380

Glu Val Glu Arg Pro Lys Leu Trp Thr Val Leu Asn Asp Lys Pro Ala
385 390 395 400

Leu Tyr Glu Leu Ile Thr Arg Val Tyr Arg Asp Gly Gln Leu Val Asp
405 410 415

Ala Lys Lys Asp Leu Phe Gly Tyr Arg Tyr Tyr His Trp Thr Pro Asn
420 425 430

Glu Gly Phe Ser Leu Asn Gly Glu Arg Ile Lys Phe His Gly Val Ser
435 440 445

Leu His His Asp His Gly Ala Leu Gly Ala Glu Glu Asn Tyr Lys Ala
450 455 460

Glu Tyr Arg Arg Leu Lys Gln Met Lys Glu Met Gly Val Asn Ser Ile
465 470 475 480

Arg Thr Thr His Asn Pro Ala Ser Glu Gln Thr Leu Gln Ile Ala Ala
485 490 495

Glu Leu Gly Leu Leu Val Gln Glu Glu Ala Phe Asp Thr Trp Tyr Gly
500 505 510

Gly Lys Lys Pro Tyr Asp Tyr Gly Arg Phe Phe Glu Lys Asp Ala Thr
515 520 525

His Pro Glu Ala Arg Lys Gly Glu Lys Trp Ser Asp Phe Asp Leu Arg
530 535 540

Thr Met Val Glu Arg Gly Lys Asn Asn Pro Ala Ile Phe Met Trp Ser
545 550 555 560

Ile Gly Asn Glu Ile Gly Glu Ala Asn Gly Asp Ala His Ser Leu Ala
565 570 575

Thr Val Lys Arg Leu Val Lys Val Ile Lys Asp Val Asp Lys Thr Arg
580 585 590

Tyr Val Thr Met Gly Ala Asp Lys Phe Arg Phe Gly Asn Gly Ser Gly
595 600 605

Gly His Glu Lys Ile Ala Asp Glu Leu Asp Ala Val Gly Phe Asn Tyr
610 615 620

Ser Glu Asp Asn Tyr Lys Ala Leu Arg Ala Lys His Pro Lys Trp Leu
625 630 635 640

Ile Tyr Gly Ser Glu Thr Ser Ser Ala Thr Arg Thr Arg Gly Ser Tyr
645 650 655

Tyr Arg Pro Glu Arg Glu Leu Lys His Ser Asn Gly Pro Glu Arg Asn
660 665 670

Tyr Glu Gln Ser Asp Tyr Gly Asn Asp Arg Val Gly Trp Gly Lys Thr
675 680 685

Ala Thr Ala Ser Trp Thr Phe Asp Arg Asp Asn Ala Gly Tyr Ala Gly
690 695 700

Gln Phe Ile Trp Thr Gly Thr Asp Tyr Ile Gly Glu Pro Thr Pro Trp
705 710 715 720

His Asn Gln Asn Gln Thr Pro Val Lys Ser Ser Tyr Phe Gly Ile Val
725 730 735

Asp Thr Ala Gly Ile Pro Lys His Asp Phe Tyr Leu Tyr Gln Ser Gln
740 745 750

Trp Val Ser Val Lys Lys Lys Pro Met Val His Leu Leu Pro His Trp
755 760 765

Asn Trp Glu Asn Lys Glu Leu Ala Ser Lys Val Ala Asp Ser Glu Gly
770 775 780

Lys Ile Pro Val Arg Ala Tyr Ser Asn Ala Ser Ser Val Glu Leu Phe
785 790 795 800

Leu Asn Gly Lys Ser Leu Gly Leu Lys Thr Phe Asn Lys Lys Gln Thr
805 810 815

Ser Asp Gly Arg Thr Tyr Gln Glu Gly Ala Asn Ala Asn Glu Leu Tyr
820 825 830

Leu Glu Trp Lys Val Ala Tyr Gln Pro Gly Thr Leu Glu Ala Ile Ala
835 840 845

Arg Asp Glu Ser Gly Lys Glu Ile Ala Arg Asp Lys Ile Thr Thr Ala
850 855 860

Gly Lys Pro Ala Ala Val Arg Leu Ile Lys Glu Asp His Ala Ile Ala
865 870 875 880

Ala Asp Gly Lys Asp Leu Thr Tyr Ile Tyr Tyr Glu Ile Val Asp Ser
885 890 895

Gln Gly Asn Val Val Pro Thr Ala Asn Asn Leu Val Arg Phe Gln Leu
900 905 910

His Gly Gln Gly Gln Leu Val Gly Val Asp Asn Gly Glu Gln Ala Ser
915 920 925

Arg Glu Arg Tyr Lys Ala Gln Ala Asp Gly Ser Trp Ile Arg Lys Ala
930 935 940

Phe Asn Gly Lys Gly Val Ala Ile Val Lys Ser Thr Glu Gln Ala Gly
945 950 955 960

Lys Phe Thr Leu Thr Ala His Ser Asp Leu Leu Lys Ser Asn Gln Val
965 970 975

Thr Val Phe Thr Gly Lys Lys Glu Gly Gln Glu Lys Thr Val Leu Gly
980 985 990

Thr Glu Val Pro Lys Val Gln Thr Ile Ile Gly Glu Ala Pro Glu Met
995 1000 1005

Pro Thr Thr Val Pro Phe Val Tyr Ser Asp Gly Ser Arg Ala Glu
1010 1015 1020

Arg Pro Val Thr Trp Ser Ser Val Asp Val Ser Lys Pro Gly Ile
1025 1030 1035

Val Thr Val Lys Gly Met Ala Asp Gly Arg Glu Val Glu Ala Arg
1040 1045 1050

Val Glu Val Ile Ala Leu Lys Ser Glu Leu Pro Val Val Lys Arg
1055 1060 1065

Ile Ala Pro Asn Thr Asp Leu Asn Ser Val Asp Lys Ser Val Ser
1070 1075 1080

Tyr Val Leu Ile Asp Gly Ser Val Glu Glu Tyr Glu Val Asp Lys
1085 1090 1095

Trp Glu Ile Ala Glu Glu Asp Lys Ala Lys Leu Ala Ile Pro Gly
1100 1105 1110

Ser Arg Ile Gln Ala Thr Gly Tyr Leu Glu Gly Gln Pro Ile His
1115 1120 1125

Ala Thr Leu Val Val Glu Glu Gly Asn Pro Ala Ala Pro Ala Val
1130 1135 1140

Pro Thr Val Thr Val Gly Gly Glu Ala Val Thr Gly Leu Thr Ser
1145 1150 1155

Gln Lys Pro Met Gln Tyr Arg Thr Leu Ala Tyr Gly Ala Lys Leu
1160 1165 1170

Pro Glu Val Thr Ala Ser Ala Lys Asn Ala Ala Val Thr Val Leu
1175 1180 1185

Gln Ala Ser Ala Ala Asn Gly Met Arg Ala Ser Ile Phe Ile Gln
1190 1195 1200

Pro Lys Asp Gly Gly Pro Leu Gln Thr Tyr Ala Ile Gln Phe Leu
1205 1210 1215

Glu Glu Ala Pro Lys Ile Ala His Leu Ser Leu Gln Val Glu Lys
1220 1225 1230

Ala Asp Ser Leu Lys Glu Asp Gln Thr Val Lys Leu Ser Val Arg
1235 1240 1245

Ala His Tyr Gln Asp Gly Thr Gln Ala Val Leu Pro Ala Asp Lys
1250 1255 1260

Val Thr Phe Ser Thr Ser Gly Glu Gly Glu Val Ala Ile Arg Lys
1265 1270 1275

Gly Met Leu Glu Leu His Lys Pro Gly Ala Val Thr Leu Asn Ala
1280 1285 1290

Glu Tyr Glu Gly Ala Lys Asp Gln Val Glu Leu Thr Ile Gln Ala
1295 1300 1305

Asn Thr Glu Lys Lys Ile Ala Gln Ser Ile Arg Pro Val Asn Val
1310 1315 1320

Val Thr Asp Leu His Gln Glu Pro Ser Leu Pro Ala Thr Val Thr
1325 1330 1335

Val Glu Tyr Asp Lys Gly Phe Pro Lys Thr His Lys Val Thr Trp
1340 1345 1350

Gln Ala Ile Pro Lys Glu Lys Leu Asp Ser Tyr Gln Thr Phe Glu
1355 1360 1365

Val Leu Gly Lys Val Glu Gly Ile Asp Leu Glu Ala Arg Ala Lys
1370 1375 1380

Val Ser Val Glu Gly Ile Val Ser Val Glu Glu Val Ser Val Thr
1385 1390 1395

Thr Pro Ile Ala Glu Ala Pro Gln Leu Pro Glu Ser Val Arg Thr
1400 1405 1410

Tyr Asp Ser Asn Gly His Val Ser Ser Ala Lys Val Ala Trp Asp
1415 1420 1425

Ala Ile Arg Pro Glu Gln Tyr Ala Lys Glu Gly Val Phe Thr Val
1430 1435 1440

Asn Gly Arg Leu Glu Gly Thr Gln Leu Thr Thr Lys Leu His Val
1445 1450 1455

Arg Val Ser Ala Gln Thr Glu Gln Gly Ala Asn Ile Ser Asp Gln
1460 1465 1470

Trp Thr Gly Ser Glu Leu Pro Leu Ala Phe Ala Ser Asp Ser Asn
1475 1480 1485

Pro Ser Asp Pro Val Ser Asn Val Asn Asp Lys Leu Ile Ser Tyr
1490 1495 1500

Asn Asn Gln Pro Ala Asn Arg Trp Thr Asn Trp Asn Arg Thr Asn
1505 1510 1515

Pro Glu Ala Ser Val Gly Val Leu Phe Gly Asp Ser Gly Ile Leu
1520 1525 1530

Ser Lys Arg Ser Val Asp Asn Leu Ser Val Gly Phe His Glu Asp
1535 1540 1545

His Gly Val Gly Val Pro Lys Ser Tyr Val Ile Glu Tyr Tyr Val
1550 1555 1560

Gly Lys Thr Val Pro Thr Ala Pro Lys Asn Pro Ser Phe Val Gly
1565 1570 1575

Asn Glu Asp His Val Phe Asn Asp Ser Ala Asn Trp Lys Pro Val
1580 1585 1590

Thr Asn Leu Lys Ala Pro Ala Gln Leu Lys Ala Gly Glu Met Asn
1595 1600 1605

His Phe Ser Phe Asp Lys Val Glu Thr Tyr Ala Val Arg Ile Arg
1610 1615 1620

Met Val Lys Ala Asp Asn Lys Arg Gly Thr Ser Ile Thr Glu Val
1625 1630 1635

Gln Ile Phe Ala Lys Gln Val Ala Ala Ala Lys Gln Gly Gln Thr
1640 1645 1650

Arg Ile Gln Val Asp Gly Lys Asp Leu Ala Asn Phe Asn Pro Asp
1655 1660 1665

Leu Thr Asp Tyr Tyr Leu Glu Ser Val Asp Gly Lys Val Pro Ala
1670 1675 1680

Val Thr Ala Ser Val Ser Asn Asn Gly Leu Ala Thr Val Val Pro
1685 1690 1695

Ser Val Arg Glu Gly Glu Pro Val Arg Val Ile Ala Lys Ala Glu
1700 1705 1710

Asn Gly Asp Ile Leu Gly Glu Tyr Arg Leu His Phe Thr Lys Asp
1715 1720 1725

Lys Ser Leu Leu Ser His Lys Pro Val Ala Ala Val Lys Gln Ala
1730 1735 1740

Arg Leu Leu Gln Val Gly Gln Ala Leu Glu Leu Pro Thr Lys Val
1745 1750 1755

Pro Val Tyr Phe Thr Gly Lys Asp Gly Tyr Glu Thr Lys Asp Leu
1760 1765 1770

Thr Val Glu Trp Glu Glu Val Pro Ala Glu Asn Leu Thr Lys Ala
1775 1780 1785

Gly Gln Phe Thr Val Arg Gly Arg Val Leu Gly Ser Asn Leu Val
1790 1795 1800

Ala Glu Ile Thr Val Arg Val Thr Asp Lys Leu Gly Glu Thr Leu
1805 1810 1815

Ser Asp Asn Pro Asn Tyr Asp Glu Asn Ser Asn Gln Ala Phe Ala
1820 1825 1830

Ser Ala Thr Asn Asp Ile Asp Lys Asn Ser His Asp Arg Val Asp
1835 1840 1845

Tyr Leu Asn Asp Gly Asp His Ser Glu Asn Arg Arg Trp Thr Asn
1850 1855 1860

Trp Ser Pro Thr Pro Ser Ser Asn Pro Glu Val Ser Ala Gly Val
1865 1870 1875

Ile Phe Arg Glu Asn Gly Lys Ile Val Glu Arg Thr Val Thr Gln
1880 1885 1890

Gly Lys Val Gln Phe Phe Ala Asp Ser Gly Thr Asp Ala Pro Ser
1895 1900 1905

Lys Leu Val Leu Glu Arg Tyr Val Gly Pro Glu Phe Glu Val Pro
1910 1915 1920

Thr Tyr Tyr Ser Asn Tyr Gln Ala Tyr Asp Ala Asp His Pro Phe
1925 1930 1935

Asn Asn Pro Glu Asn Trp Glu Ala Val Pro Tyr Arg Ala Asp Lys
1940 1945 1950

Asp Ile Ala Ala Gly Asp Glu Ile Asn Val Thr Phe Lys Ala Ile
1955 1960 1965

Lys Ala Lys Ala Met Arg Trp Arg Met Glu Arg Lys Ala Asp Lys
1970 1975 1980

Ser Gly Val Ala Met Ile Glu Met Thr Phe Leu Ala Pro Ser Glu
1985 1990 1995

Leu Pro Gln Glu Ser Thr Gln Ser Lys Ile Leu Val Asp Gly Lys
2000 2005 2010

Glu Leu Ala Asp Phe Ala Glu Asn Arg Gln Asp Tyr Gln Ile Thr
2015 2020 2025

Tyr Lys Gly Gln Arg Pro Lys Val Ser Val Glu Glu Asn Asn Gln
2030 2035 2040

Val Ala Ser Thr Val Val Asp Ser Gly Glu Asp Ser Phe Pro Val
2045 2050 2055

Leu Val Arg Leu Val Ser Glu Ser Gly Lys Gln Val Lys Glu Tyr
2060 2065 2070

Arg Ile His Leu Thr Lys Glu Lys Pro Val Ser Glu Lys Thr Val
2075 2080 2085

Ala Ala Val Gln Glu Asp Leu Pro Lys Ile Glu Phe Val Glu Lys
2090 2095 2100

Asp Leu Ala Tyr Lys Thr Val Glu Lys Lys Asp Ser Thr Leu Tyr
2105 2110 2115

Leu Gly Glu Thr Arg Val Glu Gln Glu Gly Lys Val Gly Lys Glu
2120 2125 2130

Arg Ile Phe Thr Ala Ile Asn Pro Asp Gly Ser Lys Glu Glu Lys
2135 2140 2145

Leu Arg Glu Val Val Glu Val Pro Thr Asp Arg Ile Val Leu Val
2150 2155 2160

Gly Thr Lys Pro Val Ala Gln Glu Ala Lys Lys Pro Gln Val Ser
2165 2170 2175

Glu Lys Ala Asp Thr Lys Pro Ile Asp Ser Ser Glu Ala Ser Gln
2180 2185 2190

Thr Asn Lys Ala Gln Leu Pro Ser Thr Gly Ser Ala Ala Ser Gln
2195 2200 2205

Ala Ala Val Ala Ala Gly Leu Thr Leu Leu Gly Leu Ser Ala Gly
2210 2215 2220

Leu Val Val Thr Lys Gly Lys Lys Glu Asp
2225 2230

<210> 179

<211> 1881

<212> PRT

<213> Streptococcus pneumoniae

<400> . 179

Met Ala Pro Ser Val Val Asp Ala Ala Thr Tyr His Tyr Val Asn Lys
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Glu Ile Ile Ser Gln Glu Ala Lys Asp Leu Ile Gln Thr Gly Lys Pro
20 25 30

Asp Arg Asn Glu Val Val Tyr Gly Leu Val Tyr Gln Lys Asp Gln Leu
35 40 45

Pro Gln Thr Gly Thr Glu Ala Ser Val Leu Thr Ala Phe Gly Leu Leu
50 55 60

Thr Val Gly Ser Leu Leu Leu Ile Tyr Lys Arg Lys Lys Ile Ala Ser
65 70 75 80

Val Phe Leu Val Gly Ala Met Gly Leu Val Val Leu Pro Ser Ala Gly
85 90 95

Ala Val Asp Pro Val Ala Thr Leu Ala Leu Ala Ser Arg Glu Gly Val
100 105 110

Val Glu Met Glu Gly Tyr Arg Tyr Val Gly Tyr Leu Ser Gly Asp Ile
115 120 125

Leu Lys Thr Leu Gly Leu Asp Thr Val Leu Glu Glu Thr Ser Ala Lys
130 135 140

Pro Gly Glu Val Thr Val Val Glu Val Glu Thr Pro Gln Ser Ile Thr
145 150 155 160

Asn Gln Glu Gln Ala Arg Thr Glu Asn Gln Val Val Glu Thr Glu Glu
165 170 175

Ala Pro Lys Glu Glu Ala Pro Lys Thr Glu Glu Ser Pro Lys Glu Glu
180 185 190

Pro Lys Ser Glu Val Lys Pro Thr Asp Asp Thr Leu Pro Lys Val Glu
195 200 205

Glu Gly Lys Glu Asp Ser Ala Glu Pro Ala Pro Val Glu Glu Val Gly
210 215 220

Gly Glu Val Glu Ser Lys Pro Glu Glu Lys Val Ala Val Lys Pro Glu
225 230 235 240

Ser Gln Pro Ser Asp Lys Pro Ala Glu Glu Ser Lys Val Glu Gln Ala
245 250 255

Gly Glu Pro Val Ala Pro Arg Glu Asp Glu Lys Ala Pro Val Glu Pro
260 265 270

Glu Lys Gln Pro Glu Ala Pro Glu Glu Glu Lys Ala Val Glu Glu Thr
275 280 285

Pro Lys Gln Glu Glu Ser Thr Pro Asp Thr Lys Ala Glu Glu Thr Val
290 295 300

Glu Pro Lys Glu Glu Thr Val Asn Gln Ser Ile Glu Gln Pro Lys Val
305 310 315 320

Glu Thr Pro Ala Val Glu Lys Gln Thr Glu Pro Thr Glu Glu Pro Lys
325 330 335

Val Glu Gln Ala Gly Glu Pro Val Ala Pro Arg Glu Asp Glu Gln Ala
340 345 350

Pro Thr Ala Pro Val Glu Pro Glu Lys Gln Pro Glu Val Pro Glu Glu
355 360 365

Glu Lys Ala Val Glu Glu Thr Pro Lys Pro Glu Asp Lys Ile Lys Gly
370 375 380

Ile Gly Thr Lys Glu Pro Val Asp Lys Ser Glu Leu Asn Asn Gln Ile
385 390 395 400

Asp Lys Ala Ser Ser Val Ser Pro Thr Asp Tyr Ser Thr Ala Ser Tyr
405 410 415

Asn Ala Leu Gly Pro Val Leu Glu Thr Ala Lys Gly Val Tyr Ala Ser
420 425 430

Glu Pro Val Lys Gln Pro Glu Val Asn Ser Glu Thr Asn Lys Leu Lys
435 440 445

Thr Ala Ile Asp Ala Leu Asn Val Asp Lys Thr Glu Leu Asn Asn Thr
450 455 460

Ile Ala Asp Ala Lys Thr Lys Val Lys Glu His Tyr Ser Asp Arg Ser
465 470 475 480

Trp Gln Asn Leu Gln Thr Glu Val Thr Lys Ala Glu Lys Val Ala Ala
485 490 495

Asn Thr Asp Ala Lys Gln Ser Glu Val Asn Glu Ala Val Glu Lys Leu
500 505 510

Thr Ala Thr Ile Glu Lys Leu Val Glu Leu Ser Glu Lys Pro Ile Leu
515 520 525

Thr Leu Thr Ser Thr Asp Lys Lys Ile Leu Glu Arg Glu Ala Val Ala
530 535 540

Lys Tyr Thr Leu Glu Asn Gln Asn Lys Thr Lys Ile Lys Ser Ile Thr
545 550 555 560

Ala Glu Leu Lys Lys Gly Glu Glu Val Ile Asn Thr Val Val Leu Thr
565 570 575

Asp Asp Lys Val Thr Thr Glu Thr Ile Ser Ala Ala Phe Lys Asn Leu
580 585 590

Glu Tyr Tyr Lys Glu Tyr Thr Leu Ser Thr Thr Met Ile Tyr Asp Arg
595 600 605

Gly Asn Gly Glu Glu Thr Glu Thr Leu Glu Asn Gln Asn Ile Gln Leu
610 615 620

Asp Leu Lys Lys Val Glu Leu Lys Asn Ile Lys Arg Thr Asp Leu Ile
625 630 635 640

Lys Tyr Glu Asn Gly Lys Glu Thr Asn Glu Ser Leu Ile Thr Thr Ile
645 650 655

Pro Asp Asp Lys Ser Asn Tyr Tyr Leu Lys Ile Thr Ser Asn Asn Gln
660 665 670

Lys Thr Thr Leu Leu Ala Val Lys Asn Ile Glu Glu Thr Thr Val Asn
675 680 685

Gly Thr Pro Val Tyr Lys Val Thr Ala Ile Ala Asp Asn Leu Val Ser
690 695 700

Arg Thr Ala Asp Asn Lys Phe Glu Glu Glu Tyr Val His Tyr Ile Glu
705 710 715 720

Lys Pro Lys Val His Glu Asp Asn Val Tyr Tyr Asn Phe Lys Glu Leu
725 730 735

Val Glu Ala Ile Gln Asn Asp Pro Ser Lys Glu Tyr Arg Leu Gly Gln
740 745 750

Ser Met Ser Ala Arg Asn Val Val Pro Asn Gly Lys Ser Tyr Ile Thr
755 760 765

Lys Glu Phe Thr Gly Lys Leu Leu Ser Ser Glu Gly Lys Gln Phe Ala
770 775 780

Ile Thr Glu Leu Glu His Pro Leu Phe Asn Val Ile Thr Asn Ala Thr
785 790 795 800

Ile Asn Asn Val Asn Phe Glu Asn Val Glu Ile Glu Arg Ser Gly Gln
805 810 815

Asp Asn Ile Ala Ser Leu Ala Asn Thr Met Lys Gly Ser Ser Val Ile
820 825 830

Thr Asn Val Lys Ile Thr Gly Thr Leu Ser Gly Arg Asn Asn Val Ala
835 840 845

Gly Phe Val Asn Asn Met Asn Asp Gly Thr Arg Ile Glu Asn Val Ala
850 855 860

Phe Phe Gly Lys Leu His Ser Thr Ser Gly Asn Gly Ser His Thr Gly
865   870   875   880

Gly Ile Ala Gly Thr Asn Tyr Arg Gly Ile Val Arg Lys Ala Tyr Val
                885   890   895

Asp Ala Thr Ile Thr Gly Asn Lys Thr Arg Ala Ser Leu Leu Val Pro
            900   905   910

Lys Val Asp Tyr Gly Leu Thr Leu Asp His Leu Ile Gly Thr Lys Ala
        915   920   925

Leu Leu Thr Glu Ser Val Val Lys Gly Lys Ile Asp Val Ser Asn Pro
    930   935   940

Val Glu Val Gly Ala Ile Ala Ser Lys Thr Trp Pro Val Gly Thr Val
945   950   955   960

Ser Asn Ser Val Ser Tyr Ala Lys Ile Ile Arg Gly Glu Glu Leu Phe
                965   970   975

Gly Ser Asn Asp Val Asp Asp Ser Asp Tyr Ala Ser Ala His Ile Lys
            980   985   990

Asp Leu Tyr Ala Val Glu Gly Tyr Ser Ser Gly Asn Arg Ser Phe Arg
        995   1000   1005

Lys Ser Lys Thr Phe Thr Lys Leu Thr Lys Glu Gln Ala Asp Ala
    1010   1015   1020

Lys Val Thr Thr Phe Asn Ile Thr Ala Asp Lys Leu Glu Ser Asp
    1025   1030   1035

Leu Ser Pro Leu Ala Lys Leu Asn Glu Glu Lys Ala Tyr Ser Ser
    1040   1045   1050

Ile Gln Asp Tyr Asn Ala Glu Tyr Asn Gln Ala Tyr Lys Asn Leu
    1055   1060   1065

Glu Lys Leu Ile Pro Phe Tyr Asn Lys Asp Tyr Ile Val Tyr Gln
    1070   1075   1080

Gly Asn Lys Leu Asn Lys Glu His His Leu Asn Thr Lys Glu Val
    1085   1090   1095

Leu Ser Val Thr Ala Met Asn Asn Asn Glu Phe Ile Thr Asn Leu
    1100   1105   1110

Asp Glu Ala Asn Lys Ile Ile Val His Tyr Ala Asp Gly Thr Lys
    1115   1120   1125

Asp Tyr Phe Asn Leu Ser Ser Ser Ser Glu Gly Leu Ser Asn Val
1130 1135 1140

Lys Glu Tyr Thr Ile Thr Asp Leu Gly Ile Lys Tyr Thr Pro Asn
1145 1150 1155

Ile Val Gln Lys Asp Asn Thr Thr Leu Val Asn Asp Ile Lys Ser
1160 1165 1170

Ile Leu Glu Ser Val Glu Leu Gln Ser Gln Thr Met Tyr Gln His
1175 1180 1185

Leu Asn Arg Leu Gly Asp Tyr Arg Val Asn Ala Ile Lys Asp Leu
1190 1195 1200

Tyr Leu Glu Glu Ser Phe Thr Asp Val Lys Glu Asn Leu Thr Asn
1205 1210 1215

Leu Ile Thr Lys Leu Val Gln Asn Glu Glu His Gln Leu Asn Asp
1220 1225 1230

Ser Pro Ala Ala Arg Gln Met Ile Arg Asp Lys Val Glu Lys Asn
1235 1240 1245

Lys Ala Ala Leu Leu Leu Gly Leu Thr Tyr Leu Asn Arg Tyr Tyr
1250 1255 1260

Gly Val Lys Phe Gly Asp Val Asn Ile Lys Glu Leu Met Leu Phe
1265 1270 1275

Lys Pro Asp Phe Tyr Gly Glu Lys Val Ser Val Leu Asp Arg Leu
1280 1285 1290

Ile Glu Ile Gly Ser Lys Glu Asn Asn Ile Lys Gly Ser Arg Thr
1295 1300 1305

Phe Asp Ala Phe Gly Gln Val Leu Ala Lys Tyr Thr Lys Ser Gly
1310 1315 1320

Asn Leu Asp Ala Phe Leu Asn Tyr Asn Arg Gln Leu Phe Thr Asn
1325 1330 1335

Ile Asp Asn Met Asn Asp Trp Phe Ile Asp Ala Thr Glu Asp His
1340 1345 1350

Val Tyr Ile Ala Glu Arg Ala Ser Glu Val Glu Glu Ile Lys Asn
1355 1360 1365

Ser Lys His Arg Ala Phe Asp Asn Leu Lys Arg Ser His Leu Arg
1370 1375 1380

Asn Thr Ile Leu Pro Leu Leu Asn Ile Asp Lys Ala His Leu Tyr
1385 1390 1395

Leu Ile Ser Asn Tyr Asn Ala Ile Ala Phe Gly Ser Ala Glu Arg
1400 1405 1410

Leu Gly Lys Lys Ser Leu Glu Asp Ile Lys Asp Ile Val Asn Lys
1415 1420 1425

Ala Ala Asp Gly Tyr Arg Asn Tyr Tyr Asp Phe Trp Tyr Arg Leu
1430 1435 1440

Ala Ser Asp Asn Val Lys Gln Arg Leu Leu Arg Asp Ala Val Ile
1445 1450 1455

Pro Ile Trp Glu Gly Tyr Asn Ala Pro Gly Gly Trp Val Glu Lys
1460 1465 1470

Tyr Gly Arg Tyr Asn Thr Asp Lys Val Tyr Thr Pro Leu Arg Glu
1475 1480 1485

Phe Phe Gly Pro Met Asp Lys Tyr Tyr Asn Tyr Asn Gly Thr Gly
1490 1495 1500

Ala Tyr Ala Ala Ile Tyr Pro Asn Ser Asp Asp Ile Arg Thr Asp
1505 1510 1515

Val Lys Tyr Val His Leu Glu Met Val Gly Glu Tyr Gly Ile Ser
1520 1525 1530

Val Tyr Thr His Glu Thr Thr His Val Asn Asp Arg Ala Ile Tyr
1535 1540 1545

Leu Gly Gly Phe Gly His Arg Glu Gly Thr Asp Ala Glu Ala Tyr
1550 1555 1560

Ala Gln Gly Met Leu Gln Thr Pro Val Thr Gly Ser Gly Phe Asp
1565 1570 1575

Glu Phe Gly Ser Leu Gly Ile Asn Met Val Phe Lys Arg Lys Asn
1580 1585 1590

Asp Gly Asn Gln Trp Tyr Ile Thr Asp Pro Lys Thr Leu Lys Thr
1595 1600 1605

Arg Glu Asp Ile Asn Arg Tyr Met Lys Gly Tyr Asn Asp Thr Leu
1610 1615 1620

Thr Leu Leu Asp Glu Ile Glu Ala Glu Ser Val Ile Ser Gln Gln
1625 1630 1635

Asn Lys Asp Leu Asn Ser Ala Trp Phe Lys Lys Ile Asp Arg Glu
1640 1645 1650

Tyr Arg Asp Asn Asn Lys Leu Asn Gln Trp Asp Lys Ile Arg Asn
1655 1660 1665

Leu Ser Gln Glu Glu Lys Asn Glu Leu Asn Ile Gln Ser Val Asn
1670 1675 1680

Asp Leu Val Asp Gln Gln Leu Met Thr Asn Arg Asn Pro Gly Asn
1685 1690 1695

Gly Ile Tyr Lys Pro Glu Ala Ile Ser Tyr Asn Asp Gln Ser Pro
1700 1705 1710

Tyr Val Gly Val Arg Met Met Thr Gly Ile Tyr Gly Gly Asn Thr
1715 1720 1725

Ser Lys Gly Ala Pro Gly Ala Val Ser Phe Lys His Asn Ala Phe
1730 1735 1740

Arg Leu Trp Gly Tyr Tyr Gly Tyr Glu Asn Gly Phe Leu Gly Tyr
1745 1750 1755

Ala Ser Asn Lys Tyr Lys Gln Gln Ser Lys Thr Asp Gly Glu Ser
1760 1765 1770

Val Leu Ser Asp Glu Tyr Ile Ile Lys Lys Ile Ser Asn Asn Thr
1775 1780 1785

Phe Asn Thr Ile Glu Glu Phe Lys Lys Ala Tyr Phe Lys Glu Val
1790 1795 1800

Lys Asp Lys Ala Thr Lys Gly Leu Thr Thr Phe Glu Val Asn Gly
1805 1810 1815

Ser Ser Val Ser Ser Tyr Asp Asp Leu Leu Thr Leu Phe Lys Glu
1820 1825 1830

Ala Val Lys Lys Asp Ala Glu Thr Leu Lys Gln Glu Ala Asn Gly
1835 1840 1845

Asn Lys Thr Val Ser Met Asn Asn Thr Val Lys Leu Lys Glu Ala
1850 1855 1860

Val Tyr Lys Lys Leu Leu Gln Gln Thr Asn Ser Phe Lys Thr Ser
1865 1870 1875

Ile Phe Lys
1880

<210> 180

<211> 332

<212> PRT

<213> Streptococcus pneumoniae

<400> 180

Met Asn Lys Arg Leu Phe Ser Lys Met Ser Leu Val Thr Leu Pro Ile
1   5   10   15

Leu Ala Leu Phe Ser Gln Ser Val Leu Ala Glu Glu Asn Ile His Phe
            20   25   30

Ser Ser Cys Lys Glu Ala Trp Ala Asn Gly Tyr Ser Asp Ile His Glu
        35   40   45

Gly Glu Pro Gly Tyr Ser Ala Lys Leu Asp Arg Asp His Asp Gly Val
    50   55   60

Ala Cys Glu Leu Lys Asn Ala Pro Lys Gly Ala Phe Lys Ala Lys Gln
65   70   75   80

Ser Thr Ala Ile Gln Ile Asn Thr Ser Ser Ala Thr Thr Ser Gly Trp
                85   90   95

Val Lys Gln Asp Gly Ala Trp Tyr Tyr Phe Asp Gly Asn Gly Asn Leu
            100   105   110

Val Lys Asn Ala Trp Gln Gly Ser Tyr Tyr Leu Lys Ala Asp Gly Lys
        115   120   125

Met Ala Gln Ser Glu Trp Ile Tyr Asp Ser Ser Tyr Gln Ala Trp Tyr
    130   135   140

Tyr Leu Lys Ser Asp Gly Ser Tyr Ala Lys Asn Ala Trp Gln Gly Ala
145   150   155   160

Tyr Tyr Leu Lys Ser Asn Gly Lys Met Ala Gln Gly Glu Trp Val Tyr
                165   170   175

Asp Ser Ser Tyr Gln Ala Trp Tyr Tyr Leu Lys Ser Asp Gly Ser Tyr
            180   185   190

Ala Arg Asn Ala Trp Gln Gly Asn Tyr Tyr Leu Lys Ser Asp Gly Lys
        195   200   205

Met Ala Lys Gly Glu Trp Val Tyr Asp Ala Thr Tyr Gln Ala Trp Tyr
    210   215   220

Tyr Leu Thr Ser Asp Gly Ser Tyr Ala Tyr Ser Thr Trp Gln Gly Asn
225   230   235   240

Tyr Tyr Leu Lys Ser Asp Gly Lys Met Ala Val Asn Glu Trp Val Asp
                245   250   255

Gly Gly Arg Tyr Tyr Val Gly Ala Asp Gly Val Trp Lys Glu Val Gln
            260   265   270

Ala Ser Thr Ala Ser Ser Ser Asn Asp Ser Asn Ser Glu Tyr Ser Ala
        275   280   285

Ala Leu Gly Lys Ala Lys Ser Tyr Asn Ser Leu Phe His Met Ser Lys
    290   295   300

Lys Arg Met Tyr Arg Gln Leu Thr Ser Asp Phe Asp Lys Phe Ser Asn
305   310   315   320

Asp Ala Ala Gln Tyr Ala Ile Asp His Leu Asp Asp
                325   330

<210> 181

<211> 450

<212> PRT

<213> Streptococcus pneumoniae

<400> 181

Met Lys Val Ile Asp Gln Phe Lys Asn Lys Lys Val Leu Val Leu Gly
1   5   10   15

Leu Ala Lys Ser Gly Glu Ser Ala Ala Arg Leu Leu Asp Lys Leu Gly
            20   25   30

Ala Ile Val Thr Val Asn Asp Gly Lys Pro Phe Glu Asp Asn Pro Ala
        35   40   45

Ala Gln Ser Leu Leu Glu Glu Gly Ile Lys Val Ile Thr Gly Gly His
    50   55   60

Pro Leu Glu Leu Leu Asp Glu Glu Phe Ala Leu Met Val Lys Asn Pro
65   70   75   80

Gly Ile Pro Tyr Asn Asn Pro Met Ile Glu Lys Ala Leu Ala Lys Gly
                85   90   95

Ile Pro Val Leu Thr Glu Val Glu Leu Ala Tyr Leu Ile Ser Glu Ala
            100   105   110

Pro Ile Ile Gly Ile Thr Gly Ser Asn Gly Lys Thr Thr Thr Thr Thr
115 120 125

Met Ile Gly Glu Val Leu Thr Ala Ala Gly Gln His Gly Leu Leu Ser
130 135 140

Gly Asn Ile Gly Tyr Pro Ala Ser Gln Val Ala Gln Ile Ala Ser Asp
145 150 155 160

Lys Asp Thr Leu Val Met Glu Leu Ser Ser Phe Gln Leu Met Gly Val
165 170 175

Gln Glu Phe His Pro Glu Ile Ala Val Ile Thr Asn Leu Met Pro Thr
180 185 190

His Ile Asp Tyr His Gly Ser Phe Ser Glu Tyr Val Ala Ala Lys Trp
195 200 205

Asn Ile Gln Asn Lys Met Thr Ala Ala Asp Phe Leu Val Leu Asn Phe
210 215 220

Asn Gln Asp Leu Ala Lys Asp Leu Thr Ser Lys Thr Glu Ala Thr Val
225 230 235 240

Val Pro Phe Ser Thr Leu Glu Lys Val Asp Gly Ala Tyr Leu Glu Asp
245 250 255

Gly Gln Leu Tyr Phe Arg Gly Glu Val Val Met Ala Ala Asn Glu Ile
260 265 270

Gly Val Pro Gly Ser His Asn Val Glu Asn Ala Leu Ala Thr Ile Ala
275 280 285

Val Ala Lys Leu Arg Asp Val Asp Asn Gln Thr Ile Lys Glu Thr Leu
290 295 300

Ser Ala Phe Gly Gly Val Lys His Arg Leu Gln Phe Val Asp Asp Ile
305 310 315 320

Lys Gly Val Lys Phe Tyr Asn Asp Ser Lys Ser Thr Asn Ile Leu Ala
325 330 335

Thr Gln Lys Ala Leu Ser Gly Phe Asp Asn Ser Lys Val Val Leu Ile
340 345 350

Ala Gly Gly Leu Asp Arg Gly Asn Glu Phe Asp Glu Leu Val Pro Asp
355 360 365

Ile Thr Gly Leu Lys Lys Met Val Ile Leu Gly Gln Ser Ala Glu Arg
370 375 380

Val Lys Arg Ala Ala Asp Lys Ala Gly Val Ala Tyr Val Glu Ala Thr
385 390 395 400

Asp Ile Ala Asp Ala Thr Arg Lys Ala Tyr Glu Leu Ala Thr Gln Gly
405 410 415

Asp Val Val Leu Leu Ser Pro Ala Asn Ala Ser Trp Asp Met Tyr Ala
420 425 430

Asn Phe Glu Val Arg Gly Asp Leu Phe Ile Asp Thr Val Ala Glu Leu
435 440 445

Lys Glu
450

<210> 182

<211> 386

<212> PRT

<213> Streptococcus pneumoniae

<400> 182

Met Lys Lys Lys Phe Ala Leu Ser Phe Val Ala Leu Ala Ser Val Ala
1 5 10 15

Leu Leu Ala Ala Cys Gly Glu Val Lys Ser Gly Ala Val Asn Thr Ala
20 25 30

Gly Asn Ser Val Glu Glu Lys Thr Ile Lys Ile Gly Phe Asn Phe Glu
35 40 45

Glu Ser Gly Ser Leu Ala Ala Tyr Gly Thr Ala Glu Gln Lys Gly Ala
50 55 60

Gln Leu Ala Val Asp Glu Ile Asn Ala Ala Gly Gly Ile Asp Gly Lys
65 70 75 80

Gln Ile Glu Val Val Asp Lys Asp Asn Lys Ser Glu Thr Ala Glu Ala
85 90 95

Ala Ser Val Thr Thr Asn Leu Val Thr Gln Ser Lys Val Ser Ala Val
100 105 110

Val Gly Pro Ala Thr Ser Gly Ala Thr Ala Ala Ala Val Ala Asn Ala
115 120 125

Thr Lys Ala Gly Val Pro Leu Ile Ser Pro Ser Ala Thr Gln Asp Gly
130 135 140

Leu Thr Lys Gly Gln Asp Tyr Leu Phe Ile Gly Thr Phe Gln Asp Ser
145   150   155   160

Phe Gln Gly Lys Ile Ile Ser Asn Tyr Val Ser Glu Lys Leu Asn Ala
                165   170   175

Lys Lys Val Val Leu Tyr Thr Asp Asn Ala Ser Asp Tyr Ala Lys Gly
            180   185   190

Ile Ala Lys Ser Phe Arg Glu Ser Tyr Lys Gly Glu Ile Val Ala Asp
        195   200   205

Glu Thr Phe Val Ala Gly Asp Thr Asp Phe Gln Ala Ala Leu Thr Lys
    210   215   220

Met Lys Gly Lys Asp Phe Asp Ala Ile Val Val Pro Gly Tyr Tyr Asn
225   230   235   240

Glu Ala Gly Lys Ile Val Asn Gln Ala Arg Gly Met Gly Ile Asp Lys
                245   250   255

Pro Ile Val Gly Gly Asp Gly Phe Asn Gly Glu Glu Phe Val Gln Gln
            260   265   270

Ala Thr Ala Glu Lys Ala Ser Asn Ile Tyr Phe Ile Ser Gly Phe Ser
        275   280   285

Thr Thr Val Glu Val Ser Ala Lys Ala Lys Ala Phe Leu Asp Ala Tyr
    290   295   300

Arg Ala Lys Tyr Asn Glu Glu Pro Ser Thr Phe Ala Ala Leu Ala Tyr
305   310   315   320

Asp Ser Val His Leu Val Ala Asn Ala Ala Lys Gly Ala Lys Asn Ser
                325   330   335

Gly Glu Ile Lys Asn Asn Leu Ala Lys Thr Lys Asp Phe Glu Gly Val
            340   345   350

Thr Gly Gln Thr Ser Phe Asp Ala Asp His Asn Thr Val Lys Thr Ala
        355   360   365

Tyr Met Met Thr Met Asn Asn Gly Lys Val Glu Ala Ala Glu Val Val
    370   375   380

Lys Pro
385

<210> 183

<211> 513

<212> PRT

<213> Streptococcus pneumoniae

<400> 183

Met Ser Ile Leu Glu Val Lys Asn Leu Ser His Gly Phe Gly Asp Arg
1 5 10 15

Ala Ile Phe Glu Asp Val Ser Phe Arg Leu Leu Lys Gly Glu His Ile
20 25 30

Gly Leu Val Gly Ala Asn Gly Glu Gly Lys Ser Thr Phe Met Ser Ile
35 40 45

Val Thr Gly Lys Met Leu Pro Asp Glu Gly Lys Val Glu Trp Ser Lys
50 55 60

Tyr Val Thr Ala Gly Tyr Leu Asp Gln His Ser Val Leu Ala Glu Arg
65 70 75 80

Gln Ser Val Arg Asp Val Leu Arg Thr Ala Phe Asp Glu Leu Phe Lys
85 90 95

Ala Glu Ala Arg Ile Asn Asp Leu Tyr Met Lys Met Ala Glu Asp Gly
100 105 110

Ala Asp Val Asp Ala Leu Met Glu Glu Val Gly Glu Leu Gln Asp Arg
115 120 125

Leu Glu Ser Arg Asp Phe Tyr Thr Leu Asp Ala Lys Ile Asp Glu Val
130 135 140

Ala Arg Ala Leu Gly Val Met Asp Phe Gly Met Asp Thr Asp Val Thr
145 150 155 160

Ser Leu Ser Gly Gly Gln Arg Thr Lys Val Leu Leu Ala Lys Leu Leu
165 170 175

Leu Glu Lys Pro Asp Ile Leu Leu Leu Asp Glu Pro Thr Asn Tyr Leu
180 185 190

Asp Ala Glu His Ile Asp Trp Leu Lys Arg Tyr Leu Gln Asn Tyr Glu
195 200 205

Asn Ala Phe Val Leu Ile Ser His Asp Ile Pro Phe Leu Asn Asp Val
210 215 220

Ile Asn Ile Val Tyr His Val Glu Asn Gln Gln Leu Thr Arg Tyr Ser
225 230 235 240

Gly Asp Tyr Tyr Gln Phe Gln Glu Val Tyr Ala Met Lys Lys Ser Gln
245 250 255

Leu Glu Ala Ala Tyr Glu Arg Gln Gln Lys Glu Ile Ala Asp Leu Lys
260 265 270

Asp Phe Val Ala Arg Asn Lys Ala Arg Val Ala Thr Arg Asn Met Ala
275 280 285

Met Ser Arg Gln Lys Lys Leu Asp Lys Met Asp Ile Ile Glu Leu Gln
290 295 300

Ser Glu Lys Pro Lys Pro Ser Phe Asp Phe Lys Pro Ala Arg Thr Pro
305 310 315 320

Gly Arg Phe Ile Phe Gln Ala Lys Asn Leu Gln Ile Gly Tyr Asp Arg
325 330 335

Pro Leu Thr Lys Pro Leu Asn Leu Thr Phe Glu Arg Asn Gln Lys Val
340 345 350

Ala Ile Ile Gly Ala Asn Gly Ile Gly Lys Thr Thr Leu Leu Lys Ser
355 360 365

Leu Leu Gly Ile Ile Ser Pro Ile Ala Gly Glu Val Glu Arg Gly Asp
370 375 380

Tyr Leu Glu Leu Gly Tyr Phe Glu Gln Glu Val Glu Gly Gly Asn Arg
385 390 395 400

Gln Thr Pro Leu Glu Ala Val Trp Asn Ala Phe Pro Ala Leu Asn Gln
405 410 415

Ala Glu Val Arg Ala Ala Leu Ala Arg Cys Gly Leu Thr Thr Lys His
420 425 430

Ile Glu Ser Gln Ile Gln Val Leu Ser Gly Gly Glu Gln Ala Lys Val
435 440 445

Arg Phe Cys Leu Leu Met Asn Arg Glu Asn Asn Val Leu Val Leu Asp
450 455 460

Glu Pro Thr Asn His Leu Asp Val Asp Ala Lys Asp Glu Leu Lys Arg
465 470 475 480

Ala Leu Lys Glu Tyr Arg Gly Ser Ile Leu Met Val Cys His Glu Pro
485 490 495

Asp Phe Tyr Glu Gly Trp Ile Asp Gln Ile Trp Asp Phe Asn Asn Leu
500 505 510

Thr

<210> 184

<211> 399

<212> PRT

<213> Streptococcus pneumoniae

<400> 184

Met Lys Lys Lys Asn Gly Lys Ala Lys Lys Trp Gln Leu Tyr Ala Ala
1 5 10 15

Ile Gly Ala Ala Ser Val Val Val Leu Gly Ala Gly Gly Ile Leu Leu
20 25 30

Phe Arg Gln Pro Ser Gln Thr Ala Leu Lys Asp Glu Pro Thr His Leu
35 40 45

Val Val Ala Lys Glu Gly Ser Val Ala Ser Ser Val Leu Leu Ser Gly
50 55 60

Thr Val Thr Ala Lys Asn Glu Gln Tyr Val Tyr Phe Asp Ala Ser Lys
65 70 75 80

Gly Asp Leu Asp Glu Ile Leu Val Ser Val Gly Asp Lys Val Ser Glu
85 90 95

Gly Gln Ala Leu Val Lys Tyr Ser Ser Ser Glu Ala Gln Ala Ala Tyr
100 105 110

Asp Ser Ala Ser Arg Ala Val Ala Arg Ala Asp Arg His Ile Asn Glu
115 120 125

Leu Asn Gln Ala Arg Asn Glu Ala Ala Ser Ala Pro Ala Pro Gln Leu
130 135 140

Pro Ala Pro Val Gly Gly Glu Asp Ala Thr Val Gln Ser Pro Thr Pro
145 150 155 160

Val Ala Gly Asn Ser Val Ala Ser Ile Asp Ala Gln Leu Gly Asp Ala
165 170 175

Arg Asp Ala Arg Ala Asp Ala Ala Ala Gln Leu Ser Lys Ala Gln Ser
180 185 190

Gln Leu Asp Ala Thr Thr Val Leu Ser Thr Leu Glu Gly Thr Val Val
195 200 205

Glu Val Asn Ser Asn Val Ser Lys Ser Pro Thr Gly Ala Ser Gln Val
210 215 220

Met Val His Ile Val Ser Asn Glu Asn Leu Gln Val Lys Gly Glu Leu
225 230 235 240

Ser Glu Tyr Asn Leu Ala Asn Leu Ser Val Gly Gln Glu Val Ser Phe
245 250 255

Thr Ser Lys Val Tyr Pro Asp Lys Lys Trp Thr Gly Lys Leu Ser Tyr
260 265 270

Ile Ser Asp Tyr Pro Lys Asn Asn Gly Glu Ala Ala Ser Pro Ala Ala
275 280 285

Gly Asn Asn Thr Gly Ser Lys Tyr Pro Tyr Thr Ile Asp Val Thr Gly
290 295 300

Glu Val Gly Asp Leu Lys Gln Gly Phe Ser Val Asn Ile Glu Val Lys
305 310 315 320

Ser Lys Thr Lys Ala Ile Leu Val Pro Val Ser Ser Leu Val Met Asp
325 330 335

Asp Ser Lys Asn Tyr Val Trp Ile Val Asp Glu Gln Gln Lys Ala Lys
340 345 350

Lys Val Glu Val Ser Leu Gly Asn Ala Asp Ala Glu Asn Gln Glu Ile
355 360 365

Thr Ser Gly Leu Thr Asn Gly Ala Lys Val Ile Ser Asn Pro Thr Ser
370 375 380

Ser Leu Glu Glu Gly Lys Glu Val Lys Ala Asp Glu Ala Thr Asn
385 390 395

<210> 185

<211> 230

<212> PRT

<213> Streptococcus pneumoniae

<400> 185

Ser Glu Thr Asn His Glu Ile Asp Ser Asn Phe Ala Gly Arg Leu Asn
1 5 10 15

Ile Leu Arg Ala Gly Val Leu Asp Ala Asn Asp Gly Ile Ile Ser Ile
20 25 30

Ala Gly Val Val Ile Gly Val Ala Ser Ala Thr Thr Asn Ile Trp Ile
35 40 45

Ile Phe Leu Ser Gly Phe Thr Ala Ile Leu Ala Gly Ala Phe Ser Met
50 55 60

Ala Gly Gly Glu Tyr Val Ser Val Ser Thr Pro Lys Asp Thr Glu Glu
65 70 75 80

Ala Ala Val Ser Arg Glu Lys Leu Leu Leu Asp Gln Asp Arg Glu Leu
85 90 95

Ala Lys Lys Ser Leu Tyr Ala Ala Tyr Ile Gln Asn Gly Glu Phe Lys
100 105 110

Thr Ser Ala Gln Leu Leu Thr Asn Lys Ile Phe Leu Lys Asn Pro Leu
115 120 125

Lys Ala Leu Val Glu Glu Lys Tyr Gly Ile Glu Tyr Glu Glu Phe Thr
130 135 140

Asn Pro Trp His Ala Ala Ile Ser Ser Phe Val Ala Phe Phe Leu Arg
145 150 155 160

Ser Leu Pro Pro Met Leu Ser Val Thr Ile Phe Pro Ser Asp Tyr Arg
165 170 175

Ile Pro Ala Thr Val Leu Ile Val Gly Val Ala Leu Leu Leu Thr Gly
180 185 190

Tyr Thr Ser Ala Arg Leu Gly Lys Ala Pro Thr Lys Thr Ala Met Ile
195 200 205

Arg Asn Leu Ala Ile Gly Leu Leu Thr Met Gly Val Thr Phe Leu Leu
210 215 220

Gly Gln Leu Phe Ser Ile
225 230

<210> 186

<211> 627

<212> PRT

<213> Streptococcus pneumoniae

<400> 186

Met Lys Lys Lys Leu Thr Ser Leu Ala Leu Val Gly Ala Phe Leu Gly
1 5 10 15

Leu Ser Trp Tyr Gly Asn Val Gln Ala Gln Glu Ser Ser Gly Asn Lys
20 25 30

Ile His Phe Ile Asn Val Gln Glu Gly Gly Ser Asp Ala Ile Ile Leu
35 40 45

Glu Ser Asn Gly His Phe Ala Met Val Asp Thr Gly Glu Asp Tyr Asp
50 55 60

Phe Pro Asp Gly Ser Asp Ser Arg Tyr Pro Trp Arg Glu Gly Ile Glu
65 70 75 80

Thr Ser Tyr Lys His Val Leu Thr Asp Arg Val Phe Arg Arg Leu Lys
85 90 95

Glu Leu Gly Val Gln Lys Leu Asp Phe Ile Leu Val Thr His Thr His
100 105 110

Ser Asp His Ile Gly Asn Val Asp Glu Leu Leu Ser Thr Tyr Pro Val
115 120 125

Asp Arg Val Tyr Leu Lys Lys Tyr Ser Asp Ser Arg Ile Thr Asn Ser
130 135 140

Glu Arg Leu Trp Asp Asn Leu Tyr Gly Tyr Asp Lys Val Leu Gln Thr
145 150 155 160

Ala Ala Glu Lys Gly Val Ser Val Ile Gln Asn Ile Thr Gln Gly Asp
165 170 175

Ala His Phe Gln Phe Gly Asp Met Asp Ile Gln Leu Tyr Asn Tyr Glu
180 185 190

Asn Glu Thr Asp Ser Ser Gly Glu Leu Lys Lys Ile Trp Asp Asp Asn
195 200 205

Ser Asn Ser Leu Ile Ser Val Val Lys Val Asn Gly Lys Lys Ile Tyr
210 215 220

Leu Gly Gly Asp Leu Asp Asn Val His Gly Ala Glu Asp Lys Tyr Gly
225 230 235 240

Pro Leu Ile Gly Lys Val Asp Leu Met Lys Phe Asn His His His Asp
245 250 255

Thr Asn Lys Ser Asn Thr Lys Asp Phe Ile Lys Asn Leu Ser Pro Ser
260 265 270

Leu Ile Val Gln Thr Ser Asp Ser Leu Pro Trp Lys Asn Gly Val Asp
275 280 285

Ser Glu Tyr Val Asn Trp Leu Lys Glu Arg Gly Ile Glu Arg Ile Asn
290 295 300

Ala Ala Ser Lys Asp Tyr Asp Ala Thr Val Phe Asp Ile Arg Lys Asp
305 310 315 320

Gly Phe Val Asn Ile Ser Thr Ser Tyr Lys Pro Ile Pro Ser Phe Gln
325 330 335

Ala Gly Trp His Lys Ser Ala Tyr Gly Asn Trp Trp Tyr Gln Ala Pro
340 345 350

Asp Ser Thr Gly Glu Tyr Ala Val Gly Trp Asn Glu Ile Glu Gly Glu
355 360 365

Trp Tyr Tyr Phe Asn Gln Thr Gly Ile Leu Leu Gln Asn Gln Trp Lys
370 375 380

Lys Trp Asn Asn His Trp Phe Tyr Leu Thr Asp Ser Gly Ala Ser Ala
385 390 395 400

Lys Asn Trp Lys Lys Ile Ala Gly Ile Trp Tyr Tyr Phe Asn Lys Glu
405 410 415

Asn Gln Met Glu Ile Gly Trp Ile Gln Asp Lys Glu Gln Trp Tyr Tyr
420 425 430

Leu Asp Val Asp Gly Ser Met Lys Thr Gly Trp Leu Gln Tyr Met Gly
435 440 445

Gln Trp Tyr Tyr Phe Ala Pro Ser Gly Glu Met Lys Met Gly Trp Val
450 455 460

Lys Asp Lys Glu Thr Trp Tyr Tyr Met Asp Ser Thr Gly Val Met Lys
465 470 475 480

Thr Gly Glu Ile Glu Val Ala Gly Gln His Tyr Tyr Leu Glu Asp Ser
485 490 495

Gly Ala Met Lys Gln Gly Trp His Lys Lys Ala Asn Asp Trp Tyr Phe
500 505 510

Tyr Lys Thr Asp Gly Ser Arg Ala Val Gly Trp Ile Lys Asp Lys Asp
515 520 525

Lys Trp Tyr Phe Leu Lys Glu Asn Gly Gln Leu Leu Val Asn Gly Lys
530 535 540

Thr Pro Glu Gly Tyr Thr Val Asp Ser Ser Gly Ala Trp Leu Val Asp
545 550 555 560

Val Ser Ile Glu Lys Ser Ala Thr Ile Lys Thr Thr Ser His Ser Glu
565 570 575

Ile Lys Glu Ser Lys Glu Val Val Lys Lys Asp Leu Glu Asn Lys Glu
580 585 590

Thr Ser Gln His Glu Ser Val Thr Asn Phe Ser Thr Ser Gln Asp Leu
595 600 605

Thr Ser Ser Thr Ser Gln Ser Ser Glu Thr Ser Val Asn Lys Ser Glu
610 615 620

Ser Glu Gln
625

<210> 187

<211> 456

<212> PRT

<213> Streptococcus pneumoniae

<400> 187

Met Asp Leu Gly Pro Thr Gln Arg Gly Ile Ser Val Val Ser Gln Ser
1 5 10 15

Tyr Ile Asn Val Ile Gly Ala Gly Leu Ala Gly Ser Glu Ala Ala Tyr
20 25 30

Gln Ile Ala Glu Arg Gly Ile Pro Val Lys Leu Tyr Glu Met Arg Gly
35 40 45

Val Lys Ser Thr Pro Gln His Lys Thr Asp Asn Phe Ala Glu Leu Val
50 55 60

Cys Ser Asn Ser Leu Arg Gly Asp Ala Leu Thr Asn Ala Val Gly Leu
65 70 75 80

Leu Lys Glu Glu Met Arg Arg Leu Gly Ser Val Ile Leu Glu Ser Ala
85 90 95

Glu Ala Thr Arg Val Pro Ala Gly Gly Ala Leu Ala Val Asp Arg Asp
100 105 110

Gly Phe Ser Gln Met Val Thr Glu Lys Val Ala Asn His Pro Leu Ile
115 120 125

Glu Val Val Arg Asp Glu Ile Thr Glu Leu Pro Thr Asp Val Ile Thr
130 135 140

Val Ile Ala Thr Gly Pro Leu Thr Ser Asp Ala Leu Ala Glu Lys Ile
145 150 155 160

His Ala Leu Asn Asp Gly Ala Gly Phe Tyr Phe Tyr Asp Ala Ala Ala
165 170 175

Pro Ile Ile Asp Val Asn Thr Ile Asp Met Ser Lys Val Tyr Leu Lys
180 185 190

Ser Arg Tyr Asp Lys Gly Glu Ala Ala Tyr Leu Asn Ala Pro Met Thr
195 200 205

Lys Gln Glu Phe Met Asp Phe His Glu Ala Leu Val Asn Ala Glu Glu
210 215 220

Ala Pro Leu Ser Ser Phe Glu Lys Glu Lys Tyr Phe Glu Gly Cys Met
225 230 235 240

Pro Ile Glu Val Met Ala Lys Arg Gly Ile Lys Thr Met Leu Tyr Gly
245 250 255

Pro Met Lys Pro Val Gly Leu Glu Tyr Pro Asp Asp Tyr Thr Gly Pro
260 265 270

Arg Asp Gly Glu Phe Lys Thr Pro Tyr Ala Val Val Gln Leu Arg Gln
275 280 285

Asp Asn Ala Ala Gly Ser Leu Tyr Asn Ile Val Gly Phe Gln Thr His
290 295 300

Leu Lys Trp Gly Glu Gln Lys Arg Val Phe Gln Met Ile Pro Gly Leu
305 310 315 320

Glu Asn Ala Glu Phe Val Arg Tyr Gly Val Met His Arg Asn Ser Tyr
325 330 335

Met Asp Ser Pro Asn Leu Leu Glu Gln Thr Tyr Arg Ser Lys Lys Gln
340 345 350

Pro Asn Leu Phe Phe Ala Gly Gln Met Thr Gly Val Glu Gly Tyr Val
355 360 365

Glu Ser Ala Ala Ser Gly Leu Val Ala Gly Ile Asn Ala Ala Arg Leu
370 375 380

Phe Lys Glu Glu Ser Glu Ala Ile Phe Pro Glu Thr Thr Ala Ile Gly
385 390 395 400

Ser Leu Ala His Tyr Ile Thr His Ala Asp Ser Lys His Phe Gln Pro
405 410 415

Met Asn Val Asn Phe Gly Ile Ile Lys Glu Leu Glu Gly Glu Arg Ile
420 425 430

Arg Asp Lys Lys Ala Arg Tyr Glu Lys Ile Ala Glu Arg Ala Leu Ala
435 440 445

Asp Leu Glu Glu Phe Leu Thr Val
450 455

<210> 188

<211> 360

<212> PRT

<213> Streptococcus pneumoniae

<400> 188

Met Leu Ile Gly Ile Pro Lys Glu Ile Lys Asn Asn Glu Asn Arg Val
1 5 10 15

Ala Leu Thr Pro Ala Gly Val His Ser Leu Val Ser Arg Gly His Arg
20 25 30

Val Leu Ile Glu Thr Asn Ala Gly Leu Gly Ser Gly Phe Thr Asp Ala
35 40 45

Asp Tyr Gln Lys Gln Gly Ala Glu Ile Val Ala Thr Ala Gly Glu Ala
50 55 60

Trp Ala Ala Glu Leu Val Val Lys Val Lys Glu Ser Leu Ser Ser Glu
65 70 75 80

Tyr Gly Tyr Leu Arg Asp Asp Leu Leu Leu Phe Thr Tyr Leu His Met
85 90 95

Ala Ala Ala Pro Glu Leu Ala Asp Ala Met Leu Thr Ala Lys Thr Thr
100 105 110

Glu Thr Val Arg Asp Asn Gln Gly Gln Leu Pro Leu Leu Val Pro Met
115 120 125

Ser Glu Val Ala Gly Arg Met Ala Val Gln Ile Gly Ala His Phe Leu
130 135 140

Thr Lys Gln Ala Gly Gly Ser Gly Val Leu Leu Gly Gly Val Pro Gly
145 150 155 160

Val Pro Lys Gly Lys Val Thr Ile Ile Gly Gly Gly Val Val Gly Thr
165 170 175

His Ala Ala Arg Ile Ala Leu Gly Leu Gly Ala Gln Val Thr Ile Leu
180 185 190

Asp Ile Ser Ser Lys Arg Leu Ser Val Leu Glu Glu Val Phe Gly Ser
195 200 205

Gln Ile Gln Thr Leu Met Ser Asn Ser Phe Asn Ile Glu Ala Ser Val
210 215 220

Arg Asp Ala Asp Val Val Ile Gly Ala Ile Leu Ile Pro Gly Ala Lys
225 230 235 240

Ala Pro Glu Leu Val Thr Asp Glu Met Val Lys Gln Met Arg Pro Gly
245 250 255

Ser Val Ser Leu Thr Leu Leu Leu Thr Lys Val Ala Leu Ser Lys Gln
260 265 270

Leu Thr Val Gln Arg Thr Met Asn Pro Ser Met Lys Asn Thr Val Phe
275 280 285

Ser Thr Met Pro Leu Pro Ile Ser Leu Val Arg Leu Leu Ala Leu Gln
290 295 300

Pro Ser Pro Pro Met Ser Leu Phe Leu Ile Ser Lys Leu Trp Leu Ala
305 310 315 320

Lys Asp Ser His Lys Gln Ser Leu Lys Met Lys Ala Cys Val Lys Val
325 330 335

Leu Leu Ile Lys Val Thr Leu Thr Tyr Gln Leu Leu Lys Asp Leu Ile
340 345 350

Val Thr Thr Leu Ile Ser Met Ile
355 360

<210> 189

<211> 839

<212> PRT

<213> Streptococcus pneumoniae

<400> 189

Met Lys Ile Asn Lys Lys Tyr Leu Ala Gly Ser Val Ala Val Leu Ala
1 5 10 15

Leu Ser Val Cys Ser Tyr Glu Leu Gly Arg His Gln Ala Gly Gln Val
20 25 30

Lys Lys Glu Ser Asn Arg Val Ser Tyr Ile Asp Gly Asp Gln Ala Gly
35 40 45

Gln Lys Ala Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly
50 55 60

Ile Asn Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val
65 70 75 80

Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr
85 90 95

Asp Ala Ile Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln
100 105 110

Leu Lys Asp Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile
115 120 125

Lys Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala
130 135 140

Asp Asn Ile Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu His
145 150 155 160

Ser His Asn His Gly Gly Gly Ser Asn Asp Gln Ala Val Val Ala Ala
165 170 175

Arg Ala Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala
180 185 190

Ser Asp Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly
195 200 205

Asp His Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu
210 215 220

Ala Ala Ala Glu Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser
225 230 235 240

Ser Ser Ser Ser Tyr Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu
245 250 255

Asn His Asn Leu Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu
260 265 270

Asn Ile Ser Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu
275 280 285

Arg His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr
290 295 300

Ser Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His
305 310 315 320

Phe Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg
325 330 335

Ile Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg
340 345 350

Pro Glu Gln Pro Ser Pro Gln Ser Thr Pro Glu Pro Ser Pro Ser Pro
355 360 365

Gln Pro Ala Pro Asn Pro Gln Pro Ala Pro Ser Asn Pro Ile Asp Glu
370 375 380

Lys Leu Val Lys Glu Ala Val Arg Lys Val Gly Asp Gly Tyr Val Phe
385 390 395 400

Glu Glu Asn Gly Val Ser Arg Tyr Ile Pro Ala Lys Asp Leu Ser Ala
405 410 415

Glu Thr Ala Ala Gly Ile Asp Ser Lys Leu Ala Lys Gln Glu Ser Leu
420 425 430

Ser His Lys Leu Gly Ala Lys Lys Thr Asp Leu Pro Ser Ser Asp Arg
435 440 445

Glu Phe Tyr Asn Lys Ala Tyr Asp Leu Leu Ala Arg Ile His Gln Asp
450 455 460

Leu Leu Asp Asn Lys Gly Arg Gln Val Asp Phe Glu Ala Leu Asp Asn
465 470 475 480

Leu Leu Glu Arg Leu Lys Asp Val Pro Ser Asp Lys Val Lys Leu Val
485 490 495

Asp Asp Ile Leu Ala Phe Leu Ala Pro Ile Arg His Pro Glu Arg Leu
500 505 510

Gly Lys Pro Asn Ala Gln Ile Thr Tyr Thr Asp Asp Glu Ile Gln Val
515 520 525

Ala Lys Leu Ala Gly Lys Tyr Thr Thr Glu Asp Gly Tyr Ile Phe Asp
530 535 540

Pro Arg Asp Ile Thr Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His
545 550 555 560

Met Thr His Ser His Trp Ile Lys Lys Asp Ser Leu Ser Glu Ala Glu
565 570 575

Arg Ala Ala Ala Gln Ala Tyr Ala Lys Glu Lys Gly Leu Thr Pro Pro
580 585 590

Ser Thr Asp His Gln Asp Ser Gly Asn Thr Glu Ala Lys Gly Ala Glu
595 600 605

Ala Ile Tyr Asn Arg Val Lys Ala Ala Lys Lys Val Pro Leu Asp Arg
610 615 620

Met Pro Tyr Asn Leu Gln Tyr Thr Val Glu Val Lys Asn Gly Ser Leu
625 630 635 640

Ile Ile Pro His Tyr Asp His Tyr His Asn Ile Lys Phe Glu Trp Phe
645 650 655

Asp Glu Gly Leu Tyr Glu Ala Pro Lys Gly Tyr Thr Leu Glu Asp Leu
660 665 670

Leu Ala Thr Val Lys Tyr Tyr Val Glu His Pro Asn Glu Arg Pro His
675 680 685

Ser Asp Asn Gly Phe Gly Asn Ala Ser Asp His Val Arg Lys Asn Lys
690 695 700

Val Asp Gln Asp Ser Lys Pro Asp Glu Asp Lys Glu His Asp Glu Val
705 710 715 720

Ser Glu Pro Thr His Pro Glu Ser Asp Glu Lys Glu Asn His Ala Gly
725 730 735

Leu Asn Pro Ser Ala Asp Asn Leu Tyr Lys Pro Ser Thr Asp Thr Glu
740 745 750

Glu Thr Glu Glu Glu Ala Glu Asp Thr Thr Asp Glu Ala Glu Ile Pro
755 760 765

Gln Val Glu Asn Ser Val Ile Asn Ala Lys Ile Ala Asp Ala Glu Ala
770 775 780

Leu Leu Glu Lys Val Thr Asp Pro Ser Ile Arg Gln Asn Ala Met Glu
785 790 795 800

Thr Leu Thr Gly Leu Lys Ser Ser Leu Leu Leu Gly Thr Lys Asp Asn
805 810 815

Asn Thr Ile Ser Ala Glu Val Asp Ser Leu Leu Ala Leu Leu Lys Glu
820 825 830

Ser Gln Pro Ala Pro Ile Gln
835

<210> 190

<211> 1039

<212> PRT

<213> Streptococcus pneumoniae

<400> 190

Met Lys Phe Ser Lys Lys Tyr Ile Ala Ala Gly Ser Ala Val Ile Val
1   5   10   15

Ser Leu Ser Leu Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu
            20   25   30

Asn Lys Asp Asn Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser
        35   40   45

Gln Lys Ser Glu Asn Leu Thr Pro Asp Gln Val Ser Gln Lys Glu Gly
    50   55   60

Ile Gln Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val
65   70   75   80

Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr
                85   90   95

Asp Ala Leu Phe Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln
            100   105   110

Leu Lys Asp Ala Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Ile Ile
        115   120   125

Lys Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala
    130   135   140

Asp Asn Val Arg Thr Lys Asp Glu Ile Asn Arg Gln Lys Gln Glu His
145   150   155   160

Val Lys Asp Asn Glu Lys Val Asn Ser Asn Val Ala Val Ala Arg Ser
                165   170   175

Gln Gly Arg Tyr Thr Thr Asn Asp Gly Tyr Val Phe Asn Pro Ala Asp
            180   185   190

Ile Ile Glu Asp Thr Gly Asn Ala Tyr Ile Val Pro His Gly Gly His
        195   200   205

Tyr His Tyr Ile Pro Lys Ser Asp Leu Ser Ala Ser Glu Leu Ala Ala
    210   215   220

Ala Lys Ala His Leu Ala Gly Lys Asn Met Gln Pro Ser Gln Leu Ser
225 230 235 240

Tyr Ser Ser Thr Ala Ser Asp Asn Asn Thr Gln Ser Val Ala Lys Gly
245 250 255

Ser Thr Ser Lys Pro Ala Asn Lys Ser Glu Asn Leu Gln Ser Leu Leu
260 265 270

Lys Glu Leu Tyr Asp Ser Pro Ser Ala Gln Arg Tyr Ser Glu Ser Asp
275 280 285

Gly Leu Val Phe Asp Pro Ala Lys Ile Ile Ser Arg Thr Pro Asn Gly
290 295 300

Val Ala Ile Pro His Gly Asp His Tyr His Phe Ile Pro Tyr Ser Lys
305 310 315 320

Leu Ser Ala Leu Glu Glu Lys Ile Ala Arg Met Val Pro Ile Ser Gly
325 330 335

Thr Gly Ser Thr Val Ser Thr Asn Ala Lys Pro Asn Glu Val Val Ser
340 345 350

Ser Leu Gly Ser Leu Ser Ser Asn Pro Ser Ser Leu Thr Thr Ser Lys
355 360 365

Glu Leu Ser Ser Ala Ser Asp Gly Tyr Ile Phe Asn Pro Lys Asp Ile
370 375 380

Val Glu Glu Thr Ala Thr Ala Tyr Ile Val Arg His Gly Asp His Phe
385 390 395 400

His Tyr Ile Pro Lys Ser Asn Gln Ile Gly Gln Pro Thr Leu Pro Asn
405 410 415

Asn Ser Leu Ala Thr Pro Ser Pro Ser Leu Pro Ile Asn Pro Gly Thr
420 425 430

Ser His Glu Lys His Glu Glu Asp Gly Tyr Gly Phe Asp Ala Asn Arg
435 440 445

Ile Ile Ala Glu Asp Glu Ser Gly Phe Val Met Ser His Gly Asp His
450 455 460

Asn His Tyr Phe Phe Lys Lys Asp Leu Thr Glu Glu Gln Ile Lys Ala
465 470 475 480

Ala Gln Lys His Leu Glu Glu Val Lys Thr Ser His Asn Gly Leu Asp
485 490 495

Ser Leu Ser Ser His Glu Gln Asp Tyr Pro Ser Asn Ala Lys Glu Met
500 505 510

Lys Asp Leu Asp Lys Lys Ile Glu Glu Lys Ile Ala Gly Ile Met Lys
515 520 525

Gln Tyr Gly Val Lys Arg Glu Ser Ile Val Val Asn Lys Glu Lys Asn
530 535 540

Ala Ile Ile Tyr Pro His Gly Asp His His His Ala Asp Pro Ile Asp
545 550 555 560

Glu His Lys Pro Val Gly Ile Gly His Ser His Ser Asn Tyr Glu Leu
565 570 575

Phe Lys Pro Glu Glu Gly Val Ala Lys Lys Glu Gly Asn Lys Val Tyr
580 585 590

Thr Gly Glu Glu Leu Thr Asn Val Val Asn Leu Leu Lys Asn Ser Thr
595 600 605

Phe Asn Asn Gln Asn Phe Thr Leu Ala Asn Gly Gln Lys Arg Val Ser
610 615 620

Phe Ser Phe Pro Pro Glu Leu Glu Lys Lys Leu Gly Ile Asn Met Leu
625 630 635 640

Val Lys Leu Ile Thr Pro Asp Gly Lys Val Leu Glu Lys Val Ser Gly
645 650 655

Lys Val Phe Gly Glu Gly Val Gly Asn Ile Ala Asn Phe Glu Leu Asp
660 665 670

Gln Pro Tyr Leu Pro Gly Gln Thr Phe Lys Tyr Thr Ile Ala Ser Lys
675 680 685

Asp Tyr Pro Glu Val Ser Tyr Asp Gly Thr Phe Thr Val Pro Thr Ser
690 695 700

Leu Ala Tyr Lys Met Ala Ser Gln Thr Ile Phe Tyr Pro Phe His Ala
705 710 715 720

Gly Asp Thr Tyr Leu Arg Val Asn Pro Gln Phe Ala Val Pro Lys Gly
725 730 735

Thr Asp Ala Leu Val Arg Val Phe Asp Glu Phe His Gly Asn Ala Tyr
740 745 750

Leu Glu Asn Asn Tyr Lys Val Gly Glu Ile Lys Leu Pro Ile Pro Lys
755 760 765

Leu Asn Gln Gly Thr Thr Arg Thr Ala Gly Asn Lys Ile Pro Val Thr
770 775 780

Phe Met Ala Asn Ala Tyr Leu Asp Asn Gln Ser Thr Tyr Ile Val Glu
785 790 795 800

Val Pro Ile Leu Glu Lys Glu Asn Gln Thr Asp Lys Pro Ser Ile Leu
805 810 815

Pro Gln Phe Lys Arg Asn Lys Ala Gln Glu Asn Leu Lys Leu Asp Glu
820 825 830

Lys Val Glu Glu Pro Lys Thr Ser Glu Lys Val Glu Lys Glu Lys Leu
835 840 845

Ser Glu Thr Gly Asn Ser Thr Ser Asn Ser Thr Leu Glu Glu Val Pro
850 855 860

Thr Val Asp Pro Val Gln Glu Lys Val Ala Lys Phe Ala Glu Ser Tyr
865 870 875 880

Gly Met Lys Leu Glu Asn Val Leu Phe Asn Met Asp Gly Thr Ile Glu
885 890 895

Leu Tyr Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Met Ala Asp Phe
900 905 910

Thr Gly Glu Ala Pro Gln Gly Asn Gly Glu Asn Lys Pro Ser Glu Asn
915 920 925

Gly Lys Val Ser Thr Gly Thr Val Glu Asn Gln Pro Thr Glu Asn Lys
930 935 940

Pro Ala Asp Ser Leu Pro Glu Ala Pro Asn Glu Lys Pro Val Lys Pro
945 950 955 960

Glu Asn Ser Thr Asp Asn Gly Met Leu Asn Pro Glu Gly Asn Val Gly
965 970 975

Ser Asp Pro Met Leu Asp Pro Ala Leu Glu Glu Ala Pro Ala Val Asp
980 985 990

Pro Val Gln Glu Lys Leu Glu Lys Phe Thr Ala Ser Tyr Gly Leu Gly
995 1000 1005

Leu Asp Ser Val Ile Phe Asn Met Asp Gly Thr Ile Glu Leu Arg
1010 1015 1020

Leu Pro Ser Gly Glu Val Ile Lys Lys Asn Leu Ser Asp Leu Ile
1025 1030 1035

Ala

<210> 191

<211> 477

<212> PRT

<213> Streptococcus pneumoniae

<400> 191

Met Lys Ile Leu Phe Val Ala Ala Glu Gly Ala Pro Phe Ser Lys Thr
1   5   10   15

Gly Gly Leu Gly Asp Val Ile Gly Ala Leu Pro Lys Ser Leu Val Lys
            20   25   30

Ala Gly His Glu Val Ala Val Ile Leu Pro Tyr Tyr Asp Met Val Glu
        35   40   45

Ala Lys Phe Gly Asn Gln Ile Glu Asp Val Leu His Phe Glu Val Ser
    50   55   60

Val Gly Trp Arg Arg Gln Tyr Cys Gly Ile Lys Lys Thr Val Leu Asn
65   70   75   80

Gly Val Thr Phe Tyr Phe Ile Asp Asn Gln Tyr Tyr Phe Phe Arg Gly
                85   90   95

His Val Tyr Gly Asp Phe Asp Asp Gly Glu Arg Phe Ala Phe Phe Gln
            100   105   110

Leu Ala Ala Ile Glu Ala Met Glu Arg Ile Asp Phe Ile Pro Asp Leu
        115   120   125

Leu His Val His Asp Tyr His Thr Ala Met Ile Pro Phe Leu Leu Lys
    130   135   140

Glu Lys Tyr Arg Trp Ile Gln Ala Tyr Glu Asp Ile Glu Thr Val Leu
145   150   155   160

Thr Ile His Asn Leu Glu Phe Gln Gly Gln Phe Ser Glu Gly Met Leu
                165   170   175

Gly Asp Leu Phe Gly Val Gly Phe Glu Arg Tyr Ala Asp Gly Thr Leu
            180   185   190

Arg Trp Asn Asn Cys Leu Asn Trp Met Lys Ala Gly Ile Leu Tyr Ala
        195   200   205

Asn Arg Val Ser Thr Val Ser Pro Ser Tyr Ala His Glu Ile Met Thr
210 215 220

Ser Gln Phe Gly Cys Asn Leu Asp Gln Ile Leu Lys Met Glu Ser Gly
225 230 235 240

Lys Val Ser Gly Ile Val Asn Gly Ile Asp Ala Asp Leu Tyr Asn Pro
245 250 255

Gln Thr Asp Ala Leu Leu Asp Tyr His Phe Asn Gln Glu Asp Leu Ser
260 265 270

Gly Lys Ala Lys Asn Lys Ala Lys Leu Gln Glu Arg Val Gly Leu Pro
275 280 285

Val Arg Ala Asp Val Pro Leu Val Gly Ile Val Ser Arg Leu Thr Arg
290 295 300

Gln Lys Gly Phe Asp Val Val Val Glu Ser Leu His His Ile Leu Gln
305 310 315 320

Glu Asp Val Gln Ile Val Leu Leu Gly Thr Gly Asp Pro Ala Phe Glu
325 330 335

Gly Ala Phe Ser Trp Phe Ala Gln Ile Tyr Pro Asp Lys Leu Ser Thr
340 345 350

Asn Ile Thr Phe Asp Val Lys Leu Ala Gln Glu Ile Tyr Ala Ala Cys
355 360 365

Asp Leu Phe Leu Met Pro Ser Arg Phe Glu Pro Cys Gly Leu Ser Gln
370 375 380

Met Met Ala Met Arg Tyr Gly Thr Leu Pro Leu Val His Glu Val Gly
385 390 395 400

Gly Leu Arg Asp Thr Val Arg Ala Phe Asn Pro Ile Glu Gly Ser Gly
405 410 415

Thr Gly Phe Ser Phe Asp Asn Leu Ser Pro Tyr Trp Leu Asn Trp Thr
420 425 430

Phe Gln Thr Ala Leu Asp Leu Tyr Arg Asn His Pro Asp Ile Trp Arg
435 440 445

Asn Leu Gln Lys Gln Ala Met Glu Ser Asp Phe Ser Trp Asp Thr Ala
450 455 460

Cys Lys Ser Tyr Leu Asp Leu Tyr His Ser Leu Val Asn
465 470 475

<210> 192

<211> 2004

<212> PRT

<213> Streptococcus pneumoniae

<400> 192

Met Glu Lys Tyr Phe Gly Glu Lys Gln Glu Arg Phe Ser Phe Arg Lys
1   5   10   15

Leu Ser Val Gly Leu Val Ser Ala Thr Ile Ser Ser Leu Phe Phe Met
            20   25   30

Ser Val Leu Ala Ser Ser Ser Val Asp Ala Gln Glu Thr Ala Gly Val
        35   40   45

His Tyr Lys Tyr Val Ala Asp Ser Glu Leu Ser Ser Glu Glu Lys Lys
    50   55   60

Gln Leu Val Tyr Asp Ile Pro Thr Tyr Val Glu Asn Asp Asp Glu Thr
65   70   75   80

Tyr Tyr Leu Val Tyr Lys Leu Asn Ser Gln Asn Gln Leu Ala Glu Leu
                85   90   95

Pro Asn Thr Gly Ser Lys Asn Glu Arg Gln Ala Leu Val Ala Gly Ala
            100   105   110

Ser Leu Ala Ala Met Gly Ile Leu Ile Phe Ala Val Ser Lys Lys Lys
        115   120   125

Val Lys Asn Lys Thr Val Leu His Leu Val Leu Val Ala Gly Ile Gly
    130   135   140

Asn Gly Val Leu Val Ser Val His Ala Leu Glu Asn His Leu Leu Leu
145   150   155   160

Asn Tyr Asn Thr Asp Tyr Glu Leu Thr Ser Gly Glu Lys Leu Pro Leu
                165   170   175

Pro Lys Glu Ile Ser Gly Tyr Thr Tyr Ile Gly Tyr Ile Lys Glu Gly
            180   185   190

Lys Thr Thr Ser Glu Ser Glu Val Ser Asn Gln Lys Ser Ser Val Ala
        195   200   205

Thr Pro Thr Lys Gln Gln Lys Val Asp Tyr Asn Val Thr Pro Asn Phe
    210   215   220

Val Asp His Pro Ser Thr Val Gln Ala Ile Gln Glu Gln Thr Pro Val
225 230 235 240

Ser Ser Thr Lys Pro Thr Glu Val Gln Val Val Glu Lys Pro Phe Ser
245 250 255

Thr Glu Leu Ile Asn Pro Arg Lys Glu Glu Lys Gln Ser Ser Asp Ser
260 265 270

Gln Glu Gln Leu Ala Glu His Lys Asn Leu Glu Thr Lys Lys Glu Glu
275 280 285

Lys Ile Ser Pro Lys Glu Lys Thr Gly Val Asn Thr Leu Asn Pro Gln
290 295 300

Asp Glu Val Leu Ser Gly Gln Leu Asn Lys Pro Glu Leu Leu Tyr Arg
305 310 315 320

Glu Glu Thr Met Glu Thr Lys Ile Asp Phe Gln Glu Glu Ile Gln Glu
325 330 335

Asn Pro Asp Leu Ala Glu Gly Thr Val Arg Val Lys Gln Glu Gly Lys
340 345 350

Leu Gly Lys Lys Val Glu Ile Val Arg Ile Phe Ser Val Asn Lys Glu
355 360 365

Glu Val Ser Arg Glu Ile Val Ser Thr Ser Thr Thr Ala Pro Ser Pro
370 375 380

Arg Ile Val Glu Lys Gly Thr Lys Lys Thr Gln Val Ile Lys Glu Gln
385 390 395 400

Pro Glu Thr Gly Val Glu His Lys Asp Val Gln Ser Gly Ala Ile Val
405 410 415

Glu Pro Ala Ile Gln Pro Glu Leu Pro Glu Ala Val Val Ser Asp Lys
420 425 430

Gly Glu Pro Glu Val Gln Pro Thr Leu Pro Glu Ala Val Val Thr Asp
435 440 445

Lys Gly Glu Thr Glu Val Gln Pro Glu Ser Pro Asp Thr Val Val Ser
450 455 460

Asp Lys Gly Glu Pro Glu Gln Val Ala Pro Leu Pro Glu Tyr Lys Gly
465 470 475 480

Asn Ile Glu Gln Val Lys Pro Glu Thr Pro Val Glu Lys Thr Lys Glu
485 490 495

Gln Gly Pro Glu Lys Thr Glu Glu Val Pro Val Lys Pro Thr Glu Glu
500 505 510

Thr Pro Val Asn Pro Asn Glu Gly Thr Thr Glu Gly Thr Ser Ile Gln
515 520 525

Glu Ala Glu Asn Pro Val Gln Pro Ala Glu Glu Ser Thr Thr Asn Ser
530 535 540

Glu Lys Val Ser Pro Asp Thr Ser Ser Lys Asn Thr Gly Glu Val Ser
545 550 555 560

Ser Asn Pro Ser Asp Ser Thr Thr Ser Val Gly Glu Ser Asn Lys Pro
565 570 575

Glu His Asn Asp Ser Lys Asn Glu Asn Ser Glu Lys Thr Val Glu Glu
580 585 590

Val Pro Val Asn Pro Asn Glu Gly Thr Val Glu Gly Thr Ser Asn Gln
595 600 605

Glu Thr Glu Lys Pro Val Gln Pro Ala Glu Glu Thr Gln Thr Asn Ser
610 615 620

Gly Lys Ile Ala Asn Glu Asn Thr Gly Glu Val Ser Asn Lys Pro Ser
625 630 635 640

Asp Ser Lys Pro Pro Val Glu Glu Ser Asn Gln Pro Glu Lys Asn Gly
645 650 655

Thr Ala Thr Lys Pro Glu Asn Ser Gly Asn Thr Thr Ser Glu Asn Gly
660 665 670

Gln Thr Glu Pro Glu Pro Ser Asn Gly Asn Ser Thr Glu Asp Val Ser
675 680 685

Thr Glu Ser Asn Thr Ser Asn Ser Asn Gly Asn Glu Glu Ile Lys Gln
690 695 700

Glu Asn Glu Leu Asp Pro Asp Lys Lys Val Glu Glu Pro Glu Lys Thr
705 710 715 720

Leu Glu Leu Arg Asn Val Ser Asp Leu Glu Leu Tyr Ser Leu Ser Asn
725 730 735

Gly Thr Tyr Lys Gln His Ile Ser Leu Glu Gln Val Pro Ser Asn Pro
740 745 750

Asn Ser Tyr Phe Val Lys Val Lys Ser Ser Ser Phe Lys Asp Val Tyr
755 760 765

Leu Pro Val Ala Ser Ile Ser Glu Glu Arg Lys Asn Asp Lys Ile Leu
770 775 780

Tyr Lys Ile Thr Ala Lys Val Glu Lys Leu Gln Gln Glu Ile Glu Ser
785 790 795 800

Arg Tyr Lys Asp Asn Phe Thr Phe Tyr Leu Ala Lys Lys Gly Thr Glu
805 810 815

Glu Thr Thr Asn Phe Thr Ser Phe Ser Asn Leu Val Lys Ala Ile Asn
820 825 830

Gln Asn Pro Ser Gly Thr Tyr His Leu Ala Ala Ser Leu Asn Ala Asn
835 840 845

Glu Val Glu Leu Gly Pro Asp Glu Arg Ser Tyr Ile Lys Asp Thr Phe
850 855 860

Thr Gly Arg Leu Ile Gly Glu Lys Asp Gly Lys Asn Tyr Ala Ile Tyr
865 870 875 880

Asn Leu Lys Lys Pro Leu Phe Glu Asn Leu Ser Gly Ala Thr Val Glu
885 890 895

Lys Leu Ser Leu Lys Asn Val Ala Ile Ser Gly Lys Asp Asp Ile Gly
900 905 910

Ser Leu Ala Asn Glu Ala Gln Asn Asn Thr Lys Ile Lys Gln Val His
915 920 925

Val Asp Gly Val Leu Ala Gly Glu Arg Gly Ile Gly Gly Leu Leu Ala
930 935 940

Lys Ala Glu Gln Ser Ser Ile Thr Glu Ser Ser Phe Lys Gly Arg Ile
945 950 955 960

Ile Asn Thr Tyr Glu Thr Thr Ala Ala Tyr Asn Ile Gly Gly Met Val
965 970 975

Gly His Leu Thr Gly Asp Lys Ala Leu Leu Thr Lys Ser Lys Ala Thr
980 985 990

Val Ala Ile Ser Ser Asn Thr Asn Thr Ser Asp Gln Thr Val Gly Gly
995 1000 1005

Leu Ala Gly Leu Val Asp Arg Asp Ala Gln Ile Gln Asp Ser Tyr
1010 1015 1020

Ala Glu Gly Asp Ile Asn Asn Val Lys His Phe Gly Arg Val Ala
1025 1030 1035

Gly Val Ala Gly Asn Leu Trp Asp Arg Thr Ser Gly Asp Val Arg
1040 1045 1050

His Ala Gly Ser Leu Thr Asn Val Leu Ser Asp Val Asn Val Thr
1055 1060 1065

Asn Gly Asn Ala Ile Thr Gly Tyr His Tyr Asn Glu Met Lys Val
1070 1075 1080

Lys Asp Thr Phe Ser Ser Lys Ala Asn Arg Val Tyr Asn Val Thr
1085 1090 1095

Leu Val Lys Asp Glu Val Val Ser Lys Glu Ser Phe Glu Glu Arg
1100 1105 1110

Gly Thr Met Leu Asp Ala Ser Gln Ile Ala Ser Lys Lys Ala Glu
1115 1120 1125

Ile Asn Pro Leu Ile Leu Pro Thr Val Glu Pro Leu Ser Thr Ser
1130 1135 1140

Gly Lys Lys Asp Ser Asp Phe Ser Lys Val Ala Tyr Tyr Gln Ala
1145 1150 1155

Lys Arg Asn Leu Thr Tyr Lys Asn Ile Glu Lys Leu Leu Pro Phe
1160 1165 1170

Tyr Asn Lys Ala Thr Ile Val Lys Tyr Gly Asn Leu Val Asn Glu
1175 1180 1185

Asn Ser Leu Leu Tyr Gln Lys Glu Leu Leu Ser Ala Val Met Met
1190 1195 1200

Lys Asp Asn Gln Val Ile Thr Asp Ile Val Ser Asn Lys Gln Thr
1205 1210 1215

Ala Asn Lys Leu Leu Leu His Tyr Lys Asp Asp Leu Ser Glu Lys
1220 1225 1230

Leu Asp Leu Lys Tyr Gln Asn Asp Phe Ala Lys Leu Ala Glu Tyr
1235 1240 1245

Ser Leu Gly Asn Thr Gly Leu Leu Tyr Thr Pro Asn Gln Phe Leu
1250 1255 1260

Tyr Asp Gln Thr Ser Ile Ile Lys Gln Val Leu Pro Asp Leu Gln
1265 1270 1275

Lys Val Asp Tyr His Ser Glu Ala Ile Arg Lys Thr Leu Gly Ile
1280 1285 1290

Ser Pro Asn Val Lys Gln Thr Glu Leu Tyr Leu Glu Asp Gln Phe
1295 1300 1305

Ala Lys Thr Lys Gln Gln Leu Glu Asp Ser Leu Lys Lys Leu Leu
1310 1315 1320

Ser Ala Asp Ala Gly Leu Ala Ser Ala Asn Pro Val Thr Glu Gly
1325 1330 1335

Tyr Leu Val Asp Lys Ile Lys Arg Asn Lys Glu Ala Leu Leu Leu
1340 1345 1350

Gly Leu Thr Tyr Leu Glu Arg Trp Tyr Asn Phe Ser Tyr Gly Gln
1355 1360 1365

Val Asn Val Lys Asp Leu Val Leu Tyr His Leu Asp Phe Phe Gly
1370 1375 1380

Lys Gly Asn Ala Ser Pro Leu Asp Thr Leu Ile Glu Leu Gly Lys
1385 1390 1395

Ser Gly Phe Asn Asn Leu Leu Ala Lys Asn Asn Val Asp Thr Tyr
1400 1405 1410

Gly Ile Ser Leu Ala Ser Gln His Gly Thr Thr Asp Leu Phe Ser
1415 1420 1425

Thr Leu Glu His Tyr Arg Lys Val Phe Leu Pro Asn Thr Ser Asn
1430 1435 1440

Asn Asp Trp Phe Lys Ser Glu Thr Lys Ala Tyr Ile Val Glu Glu
1445 1450 1455

Lys Ser Thr Ile Glu Glu Val Lys Thr Lys Gln Gly Leu Ala Gly
1460 1465 1470

Thr Lys Tyr Ser Ile Gly Val Tyr Asp Arg Ile Thr Ser Ala Thr
1475 1480 1485

Trp Lys Tyr Arg Asn Met Val Leu Pro Leu Leu Thr Leu Pro Glu
1490 1495 1500

Arg Ser Val Phe Val Ile Ser Thr Met Ser Ser Leu Gly Phe Gly
1505 1510 1515

Ala Tyr Asp Arg Tyr Arg Ser Ser Asp His Lys Ala Gly Lys Ala
1520 1525 1530

Leu Asn Asp Phe Val Glu Glu Asn Ala Arg Glu Thr Ala Lys Arg
1535 1540 1545

Gln Arg Asp His Tyr Asp Tyr Trp Tyr Arg Ile Leu Asp Asp Asn
1550 1555 1560

Ala Arg Glu Lys Leu Tyr Arg Asn Ile Leu Leu Tyr Asp Ala Tyr
1565 1570 1575

Lys Phe Gly Asp Asp Asn Thr Val Gly Lys Ala Thr Glu Val Ala
1580 1585 1590

Asp Phe Asp Asn Pro Asn Pro Ala Met Gln His Phe Phe Gly Pro
1595 1600 1605

Val Gly Asn Lys Val Gly His Asn Gln His Gly Ala Tyr Ala Thr
1610 1615 1620

Gly Asp Ala Val Tyr Tyr Met Gly Tyr Arg Met Leu Asp Lys Asp
1625 1630 1635

Gly Ala Ile Thr Tyr Thr His Glu Met Thr His Asp Ser Asp Gln
1640 1645 1650

Asp Ile Tyr Leu Gly Gly Tyr Gly Arg Arg Ser Gly Leu Gly Pro
1655 1660 1665

Glu Phe Phe Ala Lys Gly Leu Leu Gln Ala Pro Asp His Pro Asp
1670 1675 1680

Asp Ala Thr Ile Thr Ile Asn Ser Ile Leu Lys His Ser Lys Ser
1685 1690 1695

Asp Ser Thr Glu Ser Arg Arg Leu Gln Val Leu Asp Pro Thr Thr
1700 1705 1710

Arg Phe Asn Asn Ala Asp Asp Leu Lys Gln Tyr Val His Asn Met
1715 1720 1725

Phe Asp Val Val Tyr Met Leu Glu Tyr Leu Glu Gly Asn Ser Ile
1730 1735 1740

Leu Lys Leu Asp Thr Asn Gln Lys Gln Gln Leu Leu Arg Lys Val
1745 1750 1755

Thr Asn Glu Tyr His Pro Asp Pro Asp Gly Asn Lys Val Tyr Ala
1760 1765 1770

Thr Asn Val Val Arg Asn Leu Thr Val Glu Glu Val Glu Arg Leu
1775 1780 1785

Arg Ser Phe Asn Asp Leu Ile Asp Asn Asn Ile Leu Ser Ser Arg
1790 1795 1800

Glu Tyr Ala Ser Gly Lys Tyr Glu Arg Asn Gly Tyr Phe Thr Ile
1805 1810 1815

Lys Leu Phe Ala Pro Ile Tyr Ala Ala Leu Ser Asn Asp Ile Gly
1820 1825 1830

Thr Pro Gly Asp Leu Met Gly Arg Arg Ile Ala Tyr Glu Leu Leu
1835 1840 1845

Ala Ala Lys Gly Phe Lys Asp Gly Met Val Pro Tyr Ile Ser Asn
1850 1855 1860

Gln Tyr Glu Glu Glu Ala Lys Gln Lys Gly Lys Thr Ile Asn Leu
1865 1870 1875

Tyr Gly Lys Thr Arg Gly Leu Val Thr Asp Asp Leu Val Leu Glu
1880 1885 1890

Lys Val Phe Asn Asn Gln Tyr His Thr Trp Ser Glu Phe Lys Lys
1895 1900 1905

Ala Met Tyr Gln Glu Arg Gln Asp Gln Phe Asp Arg Leu Asn Lys
1910 1915 1920

Val Thr Phe Asn Asp Thr Thr Gln Pro Trp Gln Thr Phe Ala Lys
1925 1930 1935

Lys Thr Thr Ser Ser Val Asp Glu Leu Gln Lys Leu Met Asp Val
1940 1945 1950

Ala Val Arg Lys Asp Ala Glu His Asn Tyr Tyr His Trp Asn Asn
1955 1960 1965

Tyr Asn Pro Asp Ile Asp Ser Glu Val His Lys Leu Lys Arg Ala
1970 1975 1980

Ile Phe Lys Ala Tyr Leu Asp Gln Thr Asn Asp Phe Arg Ser Ser
1985 1990 1995

Ile Phe Glu Asn Lys Lys
2000

<210> 193

<211> 819

<212> PRT

<213> Streptococcus pneumoniae

<400> 193

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Met Lys Ile Asn Lys Lys Tyr Leu Ala Gly Ser Val Ala Val Leu Ala
1               5                   10                  15

Leu Ser Val Cys Ser Tyr Glu Leu Gly Arg Tyr Gln Ala Gly Gln Asp
            20                  25                  30

Lys Lys Glu Ser Asn Arg Val Ala Tyr Ile Asp Gly Asp Gln Ala Gly
        35                  40                  45

Gln Lys Ala Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu Gly
    50                  55                  60

Ile Asn Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr Val
65                  70                  75                  80

Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro Tyr
                85                  90                  95

Asp Ala Ile Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr Gln
            100                 105                 110

Leu Lys Asp Ser Asp Ile Val Asn Glu Ile Lys Gly Gly Tyr Val Ile
        115                 120                 125

Lys Val Asn Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His Ala
    130                 135                 140

Asp Asn Ile Arg Thr Lys Glu Glu Ile Lys Arg Gln Lys Gln Glu Arg
145                 150                 155                 160

Ser His Asn His Asn Ser Arg Ala Asp Asn Ala Val Ala Ala Ala Arg
                165                 170                 175

Ala Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Asn Ala Ser
            180                 185                 190

Asp Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val Pro His Gly Asp
        195                 200                 205

His Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala Ser Glu Leu Ala
    210                 215                 220

Ala Ala Glu Ala Tyr Trp Asn Gly Lys Gln Gly Ser Arg Pro Ser Ser
225                 230                 235                 240

Ser Ser Ser Tyr Asn Ala Asn Pro Ala Gln Pro Arg Leu Ser Glu Asn
                245                 250                 255

His Asn Leu Thr Val Thr Pro Thr Tyr His Gln Asn Gln Gly Glu Asn
            260                 265                 270
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Ile Ser Ser Leu Leu Arg Glu Leu Tyr Ala Lys Pro Leu Ser Glu Arg
275 280 285

His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser
290 295 300

Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe
305 310 315 320

Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile
325 330 335

Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro
340 345 350

Glu Glu Pro Ser Pro Gln Pro Thr Pro Glu Pro Ser Pro Ser Pro Gln
355 360 365

Pro Ala Pro Ser Asn Pro Ile Asp Glu Lys Leu Val Lys Glu Ala Val
370 375 380

Arg Lys Val Gly Asp Gly Tyr Val Phe Glu Glu Asn Gly Val Ser Arg
385 390 395 400

Tyr Ile Pro Ala Lys Asp Leu Ser Ala Glu Thr Ala Ala Gly Ile Asp
405 410 415

Ser Lys Leu Ala Lys Gln Glu Ser Leu Ser His Lys Leu Gly Thr Lys
420 425 430

Lys Thr Asp Leu Pro Ser Ser Asp Arg Glu Phe Tyr Asn Lys Ala Tyr
435 440 445

Asp Leu Leu Ala Arg Ile His Gln Asp Leu Leu Asp Asn Lys Gly Arg
450 455 460

Gln Val Asp Phe Glu Ala Leu Asp Asn Leu Leu Glu Arg Leu Lys Asp
465 470 475 480

Val Ser Ser Asp Lys Val Lys Leu Val Glu Asp Ile Leu Ala Phe Leu
485 490 495

Ala Pro Ile Arg His Pro Glu Arg Leu Gly Lys Pro Asn Ala Gln Ile
500 505 510

Thr Tyr Thr Asp Asp Glu Ile Gln Val Ala Lys Leu Ala Gly Lys Tyr
515 520 525

Thr Thr Glu Asp Gly Tyr Ile Phe Asp Pro Arg Asp Ile Thr Ser Asp
530 535 540

Glu Gly Asp Ala Tyr Val Thr Pro His Met Thr His Ser His Trp Ile
545 550 555 560

Lys Lys Asp Ser Leu Ser Glu Ala Glu Arg Ala Ala Ala Gln Ala Tyr
565 570 575

Ala Lys Glu Lys Gly Leu Thr Pro Pro Ser Thr Asp His Gln Asp Ser
580 585 590

Gly Asn Thr Glu Ala Lys Gly Ala Glu Ala Ile Tyr Asn Arg Val Lys
595 600 605

Ala Ala Lys Lys Val Pro Leu Asp Arg Met Pro Tyr Asn Leu Gln Tyr
610 615 620

Thr Val Glu Val Lys Asn Gly Ser Leu Ile Ile Pro His Tyr Asp His
625 630 635 640

Tyr His Asn Ile Lys Phe Glu Trp Phe Asp Glu Gly Leu Tyr Glu Ala
645 650 655

Pro Lys Gly Tyr Thr Leu Glu Asp Leu Leu Ala Thr Val Lys Tyr Tyr
660 665 670

Val Glu His Pro Asn Glu Arg Pro His Ser Asp Asn Gly Phe Gly Asn
675 680 685

Ala Ser Asp His Val Gln Arg Asn Lys Asn Gly Gln Ala Asp Thr Asn
690 695 700

Gln Thr Glu Lys Pro Ser Glu Glu Lys Pro Gln Thr Glu Lys Pro Glu
705 710 715 720

Glu Glu Thr Pro Arg Glu Glu Lys Pro Gln Ser Glu Lys Pro Glu Ser
725 730 735

Pro Lys Pro Thr Glu Glu Pro Glu Glu Ser Pro Glu Glu Ser Glu Glu
740 745 750

Pro Gln Val Glu Thr Glu Lys Val Glu Glu Lys Leu Arg Glu Ala Glu
755 760 765

Asp Leu Leu Gly Lys Ile Gln Asp Pro Ile Ile Lys Ser Asn Ala Lys
770 775 780

Glu Thr Leu Thr Gly Leu Lys Asn Asn Leu Leu Phe Gly Thr Gln Asp
785 790 795 800

Asn Asn Thr Ile Met Ala Glu Ala Glu Lys Leu Leu Ala Leu Leu Lys
805 810 815

<210> 194

<211> 802

<212> PRT

<213> Streptococcus pneumoniae

<400> 194

Leu Ile Leu Ser Val Cys Ser Tyr Glu Leu Gly Leu Tyr Gln Ala Arg
1   5   10   15

Thr Val Lys Glu Asn Asn Arg Val Ser Tyr Ile Asp Gly Lys Gln Ala
            20   25   30

Thr Gln Lys Thr Glu Asn Leu Thr Pro Asp Glu Val Ser Lys Arg Glu
        35   40   45

Gly Ile Asn Ala Glu Gln Ile Val Ile Lys Ile Thr Asp Gln Gly Tyr
    50   55   60

Val Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys Val Pro
65   70   75   80

Tyr Asp Ala Ile Ile Ser Glu Glu Leu Leu Met Lys Asp Pro Asn Tyr
                85   90   95

Lys Leu Lys Asp Glu Asp Ile Val Asn Glu Val Lys Gly Gly Tyr Val
            100   105   110

Ile Lys Val Asp Gly Lys Tyr Tyr Val Tyr Leu Lys Asp Ala Ala His
        115   120   125

Ala Asp Asn Val Arg Thr Lys Glu Glu Ile Asn Arg Gln Lys Gln Glu
    130   135   140

His Ser Gln His Arg Glu Gly Gly Thr Pro Arg Asn Asp Gly Ala Val
145   150   155   160

Ala Leu Ala Arg Ser Gln Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Ile
                165   170   175

Phe Asn Ala Ser Asp Ile Ile Glu Asp Thr Gly Asp Ala Tyr Ile Val
            180   185   190

Pro His Gly Asp His Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala
        195   200   205

Ser Glu Leu Ala Ala Ala Glu Ala Phe Leu Ser Gly Arg Gly Asn Leu
210 215 220

Ser Asn Ser Arg Thr Tyr Arg Arg Gln Asn Ser Asp Asn Thr Ser Arg
225 230 235 240

Thr Asn Trp Val Pro Ser Val Ser Asn Pro Gly Thr Thr Asn Thr Asn
245 250 255

Thr Ser Asn Asn Ser Asn Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp
260 265 270

Ile Asp Ser Leu Leu Lys Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg
275 280 285

His Val Glu Ser Asp Gly Leu Val Phe Asp Pro Ala Gln Ile Thr Ser
290 295 300

Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asp His Tyr His Phe
305 310 315 320

Ile Pro Tyr Ser Gln Met Ser Glu Leu Glu Glu Arg Ile Ala Arg Ile
325 330 335

Ile Pro Leu Arg Tyr Arg Ser Asn His Trp Val Pro Asp Ser Arg Pro
340 345 350

Glu Gln Pro Ser Pro Gln Pro Thr Pro Glu Pro Ser Pro Gly Pro Gln
355 360 365

Pro Ala Pro Asn Leu Lys Ile Asp Ser Asn Ser Ser Leu Val Ser Gln
370 375 380

Leu Val Arg Lys Val Gly Glu Gly Tyr Val Phe Glu Glu Lys Gly Ile
385 390 395 400

Ser Arg Tyr Val Phe Ala Lys Asp Leu Pro Ser Glu Thr Val Lys Asn
405 410 415

Leu Glu Ser Lys Leu Ser Lys Gln Glu Ser Val Ser His Thr Leu Thr
420 425 430

Ala Lys Lys Glu Asn Val Ala Pro Arg Asp Gln Glu Phe Tyr Asp Lys
435 440 445

Ala Tyr Asn Leu Leu Thr Glu Ala His Lys Ala Leu Phe Glu Asn Lys
450 455 460

Gly Arg Asn Ser Asp Phe Gln Ala Leu Asp Lys Leu Leu Glu Arg Leu
465 470 475 480

Asn Asp Glu Ser Thr Asn Lys Glu Lys Leu Val Asp Asp Leu Leu Ala
485 490 495

Phe Leu Ala Pro Ile Thr His Pro Glu Arg Leu Gly Lys Pro Asn Ser
500 505 510

Gln Ile Glu Tyr Thr Glu Asp Glu Val Arg Ile Ala Gln Leu Ala Asp
515 520 525

Lys Tyr Thr Thr Ser Asp Gly Tyr Ile Phe Asp Glu His Asp Ile Ile
530 535 540

Ser Asp Glu Gly Asp Ala Tyr Val Thr Pro His Met Gly His Ser His
545 550 555 560

Trp Ile Gly Lys Asp Ser Leu Ser Asp Lys Glu Lys Val Ala Ala Gln
565 570 575

Ala Tyr Thr Lys Glu Lys Gly Ile Leu Pro Pro Ser Pro Asp Ala Asp
580 585 590

Val Lys Ala Asn Pro Thr Gly Asp Ser Ala Ala Ala Ile Tyr Asn Arg
595 600 605

Val Lys Gly Glu Lys Arg Ile Pro Leu Val Arg Leu Pro Tyr Met Val
610 615 620

Glu His Thr Val Glu Val Lys Asn Gly Asn Leu Ile Ile Pro His Lys
625 630 635 640

Asp His Tyr His Asn Ile Lys Phe Ala Trp Phe Asp Asp His Thr Tyr
645 650 655

Lys Ala Pro Asn Gly Tyr Thr Leu Glu Asp Leu Phe Ala Thr Ile Lys
660 665 670

Tyr Tyr Val Glu His Pro Asp Glu Arg Pro His Ser Asn Asp Gly Trp
675 680 685

Gly Asn Ala Ser Glu His Val Leu Gly Lys Lys Asp His Ser Glu Asp
690 695 700

Pro Asn Lys Asn Phe Lys Ala Asp Glu Glu Pro Val Glu Glu Thr Pro
705 710 715 720

Ala Glu Pro Glu Val Pro Gln Val Glu Thr Glu Lys Val Glu Ala Gln
725 730 735

Leu Lys Glu Ala Glu Val Leu Leu Ala Lys Val Thr Asp Ser Ser Leu
740 745 750

Lys Ala Asn Ala Thr Glu Thr Leu Ala Gly Leu Arg Asn Asn Leu Thr
        755   760   765

Leu Gln Ile Met Asp Asn Asn Ser Ile Met Ala Glu Ala Glu Lys Leu
    770   775   780

Leu Ala Leu Leu Lys Gly Ser Asn Pro Ser Ser Val Ser Lys Glu Lys
785   790   795   800

Ile Asn

<210> 195

<211> 1084

<212> PRT

<213> Streptococcus pneumoniae

<400> 195

Met Pro Val Glu Ile Lys Thr Thr Lys Glu Ile His Pro Lys Ile Tyr
1   5   10   15

Ala Tyr Thr Thr Pro Thr Val Thr Ser Asn Glu Gly Trp Ile Lys Ile
            20   25   30

Gly Tyr Thr Glu Arg Asp Val Thr Gln Arg Ile Lys Glu Gln Thr His
        35   40   45

Thr Ala His Ile Ala Thr Asp Val Leu Trp Thr Gly Asp Ala Ala Tyr
    50   55   60

Thr Glu Glu Pro Asp Lys Gly Lys Thr Phe Lys Asp His Asp Phe His
65   70   75   80

His Phe Leu Ser Phe His Asp Val Glu Arg Arg Pro Lys Thr Glu Trp
                85   90   95

Phe Tyr Phe Asn Gly Thr Pro Glu Lys Ser Lys Asn Leu Phe Asp Lys
            100   105   110

Phe Val Gln His Asp Leu Ser Gly Tyr Gln Pro Gly Lys Gly Gln Asp
        115   120   125

Tyr Thr Leu Arg Gln Glu Gln Glu Glu Ala Val Ala Lys Thr Leu Ala
    130   135   140

Tyr Phe Gln Glu His Ala Gly Gly Lys Phe Leu Trp Asn Ala Lys Pro
145   150   155   160

Arg Phe Gly Lys Thr Leu Ser Thr Tyr Asp Leu Ala Arg Arg Met Glu
165 170 175

Ala Val Asn Val Leu Ile Val Thr Asn Arg Pro Ala Ile Ala Asn Ser
180 185 190

Trp Tyr Asp Asp Phe Glu Thr Phe Ile Ala Gly Gln Thr Thr Tyr Lys
195 200 205

Phe Val Ser Glu Ser Asp Ser Leu Lys Ser Arg Pro Ile Leu Ser Arg
210 215 220

Gln Glu Phe Leu Gly Ile Leu Ala Asp Asp Val Arg Gln Leu Ala Phe
225 230 235 240

Ile Ser Leu Gln Asp Leu Lys Gly Ser Val Tyr Leu Gly Gly Glu His
245 250 255

Asp Lys Leu Lys Trp Val Thr Asp Leu His Trp Asp Leu Leu Val Ile
260 265 270

Asp Glu Ala His Glu Gly Val Asp Thr Phe Lys Thr Asp Gln Ala Phe
275 280 285

Asn Lys Ile Arg Arg Asn Phe Thr Leu His Leu Ser Gly Thr Ser Phe
290 295 300

Lys Ala Leu Ala Lys Gly Asp Phe Thr Glu Glu Gln Ile Tyr Asn Trp
305 310 315 320

Ser Tyr Ala Asp Glu Gln Ala Ala Lys Tyr Ser Trp Ser Leu Glu Gln
325 330 335

Glu Glu Glu Asn Pro Tyr Glu Ser Leu Pro Gln Leu Asn Leu Phe Thr
340 345 350

Tyr Gln Met Ser Gln Met Ile Gly Glu Lys Leu Glu Lys Gly Ala Gln
355 360 365

Ile Asp Gly Glu Asn Ile Asp Tyr Val Phe Asp Leu Ser Glu Phe Phe
370 375 380

Ala Thr Asp Asp Lys Gly Lys Phe Ile His Glu His Asp Val Arg Asn
385 390 395 400

Trp Leu Asp Thr Leu Ser Ser Asn Glu Lys Tyr Pro Phe Ser Thr Lys
405 410 415

Glu Leu Arg Asn Glu Leu Lys His Thr Phe Trp Leu Leu Glu Arg Val
420 425 430

Ala Ser Ala Lys Ala Leu Lys Ala Leu Leu Glu Glu His Pro Ile Tyr
435 440 445

Glu Asn Tyr Glu Ile Val Leu Ala Ala Gly Asp Gly Arg Met Ser Glu
450 455 460

Glu Asp Asp Lys Val Lys Leu Lys Ser Leu Asp Leu Val Arg Lys Ala
465 470 475 480

Ile Ala Glu Asn Asp Lys Thr Ile Thr Leu Ser Val Gly Gln Leu Thr
485 490 495

Thr Gly Val Thr Ile Pro Glu Trp Thr Gly Val Leu Met Leu Ser Asn
500 505 510

Leu Lys Ser Pro Ala Leu Tyr Met Gln Ala Ala Phe Arg Ala Gln Asn
515 520 525

Pro Tyr Ser Trp Ser Asp Asn Lys Gly Asn His Phe Arg Lys Glu Arg
530 535 540

Ala Tyr Val Phe Asp Phe Ala Pro Glu Arg Thr Leu Ile Leu Phe Asp
545 550 555 560

Glu Phe Ala Asn Asn Leu Leu Leu Val Thr Ala Ala Gly Arg Gly Thr
565 570 575

Ser Ala Thr Arg Glu Glu Asn Ile Arg Glu Leu Leu Asn Phe Phe Pro
580 585 590

Ile Ile Ala Glu Asp Arg Ala Gly Lys Met Val Glu Ile Asp Ala Lys
595 600 605

Ala Val Leu Thr Thr Pro Arg Gln Ile Lys Ala Arg Glu Val Leu Lys
610 615 620

Arg Gly Phe Met Ser Asn Leu Leu Phe Asp Asn Ile Ser Gly Ile Phe
625 630 635 640

Gln Ala Ser Gln Thr Val Leu Asp Ile Leu Asn Glu Leu Pro Val Glu
645 650 655

Lys Glu Gly Lys Val Gln Asp Ser Ser Asp Leu Leu Asp Phe Ser Asp
660 665 670

Val Thr Val Asp Asp Glu Gly Asn Ala Val Val Asp His Glu Ile Val
675 680 685

Val Asn Gln Gln Met Arg Leu Phe Gly Glu Lys Val Tyr Gly Leu Gly
690 695 700

Glu Ser Val Ala Glu Leu Val Thr Lys Asp Glu Glu Arg Thr Gln Lys
705 710 715 720

Gln Leu Val Asn Asp Leu Ser Lys Thr Val Ser Ser Val Ile Val Glu
725 730 735

Glu Leu Lys Ala Asp Tyr Ser Leu Lys Thr Arg Glu Thr Glu Gln Ile
740 745 750

Lys Lys Gln Ile Thr Ala Thr Leu Glu Asn Glu Ile Arg Lys Asn Asp
755 760 765

Ile Glu Arg Lys Ile Ser Glu Ala His Ile Lys Gln Glu Leu Gln Gln
770 775 780

Gln Leu Lys Glu Ala Asn Asp Lys Ala Gln Lys Asp Lys Ile Gln Glu
785 790 795 800

Asp Leu Glu Lys Arg Leu Glu Glu Asn Lys Leu Ile His Lys Glu Lys
805 810 815

Leu Glu Gln Thr Leu Lys Lys Glu Val Glu Lys Met Pro Glu Lys Phe
820 825 830

Ile Glu Gln Val Glu Ile Lys Arg Val Glu Gln Leu Lys Gln Ser Ala
835 840 845

Gln Asp Glu Ile Arg Asp His Leu Arg Gly Phe Ala Arg Thr Ile Pro
850 855 860

Ser Phe Ile Met Ala Tyr Gly Asp Gln Thr Leu Thr Leu Asp Asn Phe
865 870 875 880

Asp Ala Phe Val Pro Glu His Val Phe Tyr Glu Val Thr Gly Ile Thr
885 890 895

Ile Asp Gln Phe Arg Tyr Leu Arg Asp Gly Gly Gln Asp Phe Ala Gly
900 905 910

His Leu Phe Asp Lys Ala Thr Phe Asp Glu Ala Ile Gln Glu Phe Leu
915 920 925

Arg Lys Lys Lys Glu Leu Ala Asp Tyr Phe Lys Asp Gln Lys Glu Asp
930 935 940

Ile Phe Asp Tyr Ile Pro Pro Gln Lys Thr Asn Gln Ile Phe Thr Pro
945 950 955 960

Lys Arg Val Val Lys Arg Met Val Asp Asp Leu Glu Lys Glu Asn Pro
965 970 975

Gly Ile Phe Asp Asp Pro Ser Lys Thr Phe Ile Asp Leu Tyr Met Lys
980 985 990

Ser Gly Leu Tyr Ile Ala Glu Leu Val Lys Arg Leu Tyr Asn Ser Asn
995 1000 1005

Gly Leu Lys Glu Ala Phe Pro Asn Pro Glu Glu Arg Leu Lys His
1010 1015 1020

Ile Leu Glu Lys Gln Val Tyr Gly Phe Ala Pro Ser Glu Ile Ile
1025 1030 1035

Tyr Asn Ile Ser Thr Asn Phe Ile Phe Gly Asn Leu Ser Lys Asp
1040 1045 1050

Ile Ser Arg Lys Asn Phe Val Leu Ala Asp Thr Ile Pro Ala Ala
1055 1060 1065

Lys Glu Gly Ser Ile Gln Lys Leu Val Asp Ser Tyr Phe Glu Asn
1070 1075 1080

Asn

<210> 196

<211> 234

<212> PRT

<213> Streptococcus pneumoniae

<400> 196

Met Lys Lys Ile Leu Ile Val Asp Asp Glu Lys Pro Ile Ser Asp Ile
1 5 10 15

Ile Lys Phe Asn Met Thr Lys Glu Gly Tyr Glu Val Val Thr Ala Phe
20 25 30

Asn Gly Arg Glu Ala Leu Glu Gln Phe Glu Ala Glu Gln Pro Asp Ile
35 40 45

Ile Ile Leu Asp Leu Met Leu Pro Glu Ile Asp Gly Leu Glu Val Ala
50 55 60

Lys Thr Ile Arg Lys Thr Ser Ser Val Pro Ile Leu Met Leu Ser Ala
65 70 75 80

Lys Asp Ser Glu Phe Asp Lys Val Ile Gly Leu Glu Leu Gly Ala Asp
85 90 95

Asp Tyr Val Thr Lys Pro Phe Ser Asn Arg Glu Leu Gln Ala Arg Val
100 105 110

Lys Ala Leu Leu Arg Arg Ser Gln Pro Met Pro Val Asp Gly Gln Glu
115 120 125

Ala Asp Ser Lys Pro Gln Pro Ile Gln Ile Gly Asp Leu Glu Ile Val
130 135 140

Pro Asp Ala Tyr Val Ala Lys Lys Tyr Gly Glu Glu Leu Asp Leu Thr
145 150 155 160

His Arg Glu Phe Glu Leu Leu Tyr His Leu Ala Ser His Thr Gly Gln
165 170 175

Val Ile Thr Arg Glu His Leu Leu Glu Thr Val Trp Gly Tyr Asp Tyr
180 185 190

Phe Gly Asp Val Arg Thr Val Asp Val Thr Val Arg Arg Leu Arg Glu
195 200 205

Lys Ile Glu Asp Thr Pro Ser Arg Pro Glu Tyr Ile Leu Thr Arg Arg
210 215 220

Gly Val Gly Tyr Tyr Met Arg Asn Asn Ala
225 230

<210> 197

<211> 721

<212> PRT

<213> Streptococcus pneumoniae

<400> 197

Met Lys Lys Lys Phe Leu Ala Phe Leu Leu Ile Leu Phe Pro Ile Phe
1 5 10 15

Ser Leu Gly Ile Ala Lys Ala Glu Thr Ile Lys Ile Val Ser Asp Thr
20 25 30

Ala Tyr Ala Pro Phe Glu Phe Lys Asp Ser Asp Gln Thr Tyr Lys Gly
35 40 45

Ile Asp Val Asp Ile Ile Asn Lys Val Ala Glu Ile Lys Gly Trp Asn
50 55 60

Ile Gln Met Ser Tyr Pro Gly Phe Asp Ala Ala Val Asn Ala Val Gln
65 70 75 80

Ala Gly Gln Ala Asp Ala Ile Met Ala Gly Met Thr Lys Thr Lys Glu
85 90 95

Arg Glu Lys Val Phe Thr Met Ser Asp Thr Tyr Tyr Asp Thr Lys Val
100 105 110

Val Ile Ala Thr Thr Lys Ser His Lys Ile Ser Lys Tyr Asp Gln Leu
115 120 125

Thr Gly Lys Thr Val Gly Val Lys Asn Gly Thr Ala Ala Gln Arg Phe
130 135 140

Leu Glu Thr Ile Lys Asp Lys Tyr Gly Phe Thr Ile Lys Thr Phe Asp
145 150 155 160

Thr Gly Asp Leu Met Asn Asn Ser Leu Ser Ala Gly Ala Ile Asp Ala
165 170 175

Met Met Asp Asp Lys Pro Val Ile Glu Tyr Ala Ile Asn Gln Gly Gln
180 185 190

Asp Leu His Ile Glu Met Asp Gly Glu Ala Val Gly Ser Phe Ala Phe
195 200 205

Gly Val Lys Lys Gly Ser Lys Tyr Glu His Leu Val Thr Glu Phe Asn
210 215 220

Gln Ala Leu Ser Glu Met Lys Lys Asp Gly Ser Leu Asp Lys Ile Ile
225 230 235 240

Lys Lys Trp Thr Ala Ser Ser Ser Ser Ala Val Pro Thr Thr Thr Thr
245 250 255

Leu Ala Gly Leu Lys Ala Ile Pro Val Lys Ala Lys Tyr Ile Ile Ala
260 265 270

Ser Asp Ser Ser Phe Ala Pro Phe Val Phe Gln Asn Ser Ser Asn Gln
275 280 285

Tyr Thr Gly Ile Asp Met Glu Leu Ile Lys Ala Ile Ala Lys Asp Gln
290 295 300

Gly Phe Glu Ile Glu Ile Thr Asn Pro Gly Phe Asp Ala Ala Ile Ser
305 310 315 320

Ala Val Gln Ala Gly Gln Ala Asp Gly Ile Ile Ala Gly Met Ser Val
325 330 335

Thr Asp Ala Arg Lys Ala Thr Phe Asp Phe Ser Glu Ser Tyr Tyr Thr
340 345 350

Ala Asn Thr Ile Leu Gly Val Lys Glu Ser Ser Asn Ile Ala Ser Tyr
355 360 365

Glu Asp Leu Lys Gly Lys Thr Val Gly Val Lys Asn Gly Thr Ala Ser
370 375 380

Gln Thr Phe Leu Thr Glu Asn Gln Ser Lys Tyr Gly Tyr Lys Ile Lys
385 390 395 400

Thr Phe Ala Asp Gly Ser Ser Met Tyr Asp Ser Leu Asn Thr Gly Ala
405 410 415

Ile Asp Ala Val Met Asp Asp Glu Pro Val Leu Lys Tyr Ser Ile Ser
420 425 430

Gln Gly Gln Lys Leu Lys Thr Pro Ile Ser Gly Thr Pro Ile Gly Glu
435 440 445

Thr Ala Phe Ala Val Lys Lys Gly Ala Asn Pro Glu Leu Ile Glu Met
450 455 460

Phe Asn Asn Gly Leu Ala Asn Leu Lys Ala Asn Gly Glu Phe Gln Lys
465 470 475 480

Ile Leu Asp Lys Tyr Leu Ala Ser Glu Ser Ser Thr Ala Ser Thr Ser
485 490 495

Thr Val Asp Glu Thr Thr Leu Trp Gly Leu Leu Gln Asn Asn Tyr Lys
500 505 510

Gln Leu Leu Ser Gly Leu Gly Ile Thr Leu Ala Leu Ala Leu Ile Ser
515 520 525

Phe Ala Ile Ala Ile Val Ile Gly Ile Ile Phe Gly Met Phe Ser Val
530 535 540

Ser Pro Tyr Lys Ser Leu Arg Val Ile Ser Glu Ile Phe Val Asp Val
545 550 555 560

Ile Arg Gly Ile Pro Leu Met Ile Leu Ala Ala Phe Ile Phe Trp Gly
565 570 575

Ile Pro Asn Phe Ile Glu Ser Ile Thr Gly Gln Gln Ser Pro Ile Asn
580 585 590

Asp Phe Val Ala Gly Thr Ile Ala Leu Ser Leu Asn Ala Ala Ala Tyr
595 600 605

Ile Ala Glu Ile Val Arg Gly Gly Ile Gln Ala Val Pro Val Gly Gln
610 615 620

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Met Glu Ala Ser Arg Ser Leu Gly Ile Ser Tyr Gly Lys Thr Met Arg
625                 630                 635                 640

Lys Ile Ile Leu Pro Gln Ala Thr Lys Leu Met Leu Pro Asn Phe Val
                645                 650                 655

Asn Gln Phe Val Ile Ala Leu Lys Asp Thr Thr Ile Val Ser Ala Ile
            660                 665                 670

Gly Leu Val Glu Leu Phe Gln Thr Gly Lys Ile Ile Ile Ala Arg Asn
        675                 680                 685

Tyr Gln Ser Phe Lys Met Tyr Ala Ile Leu Ala Ile Phe Tyr Leu Val
    690                 695                 700

Ile Ile Thr Leu Leu Thr Arg Leu Ala Lys Arg Leu Glu Lys Arg Ile
705                 710                 715                 720

Arg
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<210> 198

<211> 523

<212> PRT

<213> Streptococcus pneumoniae

<400> 198

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Met Ala Phe Glu Ser Leu Thr Glu Arg Leu Gln Asn Val Phe Lys Asn
1               5                   10                  15

Leu Arg Lys Lys Gly Lys Ile Ser Glu Ser Asp Val Gln Glu Ala Thr
            20                  25                  30

Lys Glu Ile Arg Leu Ala Leu Leu Glu Ala Asp Val Ala Leu Pro Val
        35                  40                  45

Val Lys Asp Phe Ile Lys Lys Val Arg Glu Arg Ala Val Gly His Glu
    50                  55                  60

Val Ile Asp Thr Leu Asn Pro Ala Gln Gln Ile Ile Lys Ile Val Asp
65                  70                  75                  80

Glu Glu Leu Thr Ala Val Leu Gly Ser Asp Thr Ala Glu Ile Ile Lys
                85                  90                  95

Ser Pro Lys Ile Pro Thr Ile Ile Met Met Val Gly Leu Gln Gly Ala
            100                 105                 110
```

Gly Lys Thr Thr Phe Ala Gly Lys Leu Ala Asn Lys Leu Lys Lys Glu
115 120 125

Glu Asn Ala Arg Pro Leu Met Ile Ala Ala Asp Ile Tyr Arg Pro Ala
130 135 140

Ala Ile Asp Gln Leu Lys Thr Leu Gly Gln Gln Ile Asp Val Pro Val
145 150 155 160

Phe Ala Leu Gly Thr Glu Val Pro Ala Val Glu Ile Val Arg Gln Gly
165 170 175

Leu Glu Gln Ala Gln Thr Asn His Asn Asp Tyr Val Leu Ile Asp Thr
180 185 190

Ala Gly Arg Leu Gln Ile Asp Glu Leu Leu Met Asn Glu Leu Arg Asp
195 200 205

Val Lys Ala Leu Ala Gln Pro Asn Glu Ile Leu Leu Val Val Asp Ala
210 215 220

Met Ile Gly Gln Glu Ala Ala Asn Val Ala Arg Glu Phe Asn Ala Gln
225 230 235 240

Leu Glu Val Thr Gly Val Ile Leu Thr Lys Ile Asp Gly Asp Thr Arg
245 250 255

Gly Gly Ala Ala Leu Ser Val Arg His Ile Thr Gly Lys Pro Ile Lys
260 265 270

Phe Thr Gly Thr Gly Glu Lys Ile Thr Asp Ile Glu Thr Phe His Pro
275 280 285

Asp Arg Met Ser Ser Arg Ile Leu Gly Met Gly Asp Met Leu Thr Leu
290 295 300

Ile Glu Lys Ala Ser Gln Glu Tyr Asp Glu Gln Lys Ala Leu Glu Met
305 310 315 320

Ala Glu Lys Met Arg Glu Asn Thr Phe Asp Phe Asn Asp Phe Ile Asp
325 330 335

Gln Leu Asp Gln Val Gln Asn Met Gly Pro Met Glu Asp Leu Leu Lys
340 345 350

Met Ile Pro Gly Met Ala Asn Asn Pro Ala Leu Gln Asn Met Lys Val
355 360 365

Asp Glu Arg Gln Ile Ala Arg Lys Arg Ala Ile Val Ser Ser Met Thr
370 375 380

Pro Glu Glu Arg Glu Asn Pro Asp Leu Leu Asn Pro Ser Arg Arg Arg
385 390 395 400

Arg Ile Ala Ala Gly Ser Gly Asn Thr Phe Val Glu Val Asn Lys Phe
405 410 415

Ile Lys Asp Phe Asn Gln Ala Lys Gln Leu Met Gln Gly Val Met Ser
420 425 430

Gly Asp Met Asn Lys Met Met Lys Gln Met Gly Ile Asn Pro Asn Asn
435 440 445

Leu Pro Lys Asn Met Pro Asn Met Gly Gly Met Asp Met Ser Ala Leu
450 455 460

Glu Gly Met Met Gly Gln Gly Gly Met Pro Asp Leu Ser Ala Leu Gly
465 470 475 480

Gly Ala Gly Met Pro Asp Met Ser Gln Met Phe Gly Gly Gly Leu Lys
485 490 495

Gly Lys Ile Gly Glu Phe Ala Met Lys Gln Ser Met Lys Arg Met Ala
500 505 510

Asn Lys Met Lys Lys Ala Lys Lys Lys Arg Lys
515 520

<210> 199

<211> 233

<212> PRT

<213> Streptococcus pneumoniae

<400> 199

Met Ser Gln Ile Trp Thr Lys Glu Lys Phe Ile Ser Gln Val Gln Gly
1 5 10 15

Gly Val Ile Val Ser Cys Gln Ala Leu Pro Gly Glu Ala Leu Tyr Asn
20 25 30

Glu Glu Phe Ser Leu Met Pro Phe Met Ala Lys Ala Ala Leu Glu Ala
35 40 45

Gly Ala Val Gly Ile Arg Ala Asn Ser Val Arg Asp Ile Lys Ala Ile
50 55 60

Gln Lys Val Val Asp Leu Pro Ile Ile Gly Ile Ile Lys Arg Asp Tyr
65 70 75 80

Pro Pro Gln Glu Pro Tyr Ile Thr Ala Thr Met Lys Glu Val Asp Glu
85 90 95

Leu Val Glu Cys Gly Thr Thr Val Ile Ala Phe Asp Ala Thr Leu Arg
100 105 110

Pro Arg Tyr Asp Gly Leu Val Val Ser Glu Phe Ile Lys Lys Ile Lys
115 120 125

Glu Lys Tyr Pro Asn Gln Leu Leu Met Ala Asp Val Ser Asn Leu Asp
130 135 140

Glu Gly Leu Tyr Ala Phe Lys Ser Gly Val Asp Phe Val Gly Thr Thr
145 150 155 160

Leu Ser Gly Tyr Thr Ser Thr Ser Val Gln Ser Asp Glu Pro Asp Phe
165 170 175

Glu Leu Met Lys Lys Leu Ala Asp Phe Asn Ile Pro Val Ile Ala Glu
180 185 190

Gly Lys Ile His Tyr Pro Glu Gln Leu Lys Lys Ala Tyr Ser Leu Gly
195 200 205

Val Thr Ser Val Val Ile Gly Gly Ala Ile Thr Arg Pro Lys Glu Ile
210 215 220

Ala Gln Arg Phe Ile Asn Val Ile Lys
225 230

<210> 200

<211> 388

<212> PRT

<213> Streptococcus pneumoniae

<400> 200

Met Arg Tyr Leu Thr Ala Gly Glu Ser His Gly Pro Arg Leu Thr Ala
1 5 10 15

Ile Ile Glu Gly Ile Pro Ala Gly Leu Pro Leu Thr Ala Glu Asp Ile
20 25 30

Asn Glu Asp Leu Arg Arg Arg Gln Gly Gly Tyr Gly Arg Gly Gly Arg
35 40 45

Met Lys Ile Glu Asn Asp Gln Val Val Phe Thr Ser Gly Val Arg His
50 55 60

Gly Lys Thr Thr Gly Ala Pro Ile Thr Met Asp Val Ile Asn Lys Asp
65 70 75 80

His Gln Lys Trp Leu Asp Ile Met Ser Ala Glu Asp Ile Glu Asp Arg
85 90 95

Leu Lys Ser Lys Arg Lys Ile Thr His Pro Arg Pro Gly His Ala Asp
100 105 110

Leu Val Gly Gly Ile Lys Tyr Arg Phe Asp Asp Leu Arg Asn Ser Leu
115 120 125

Glu Arg Ser Ser Ala Arg Glu Thr Thr Met Arg Val Ala Val Gly Ala
130 135 140

Val Ala Lys Arg Leu Leu Ala Glu Leu Asp Met Glu Ile Ala Asn His
145 150 155 160

Val Val Val Phe Gly Gly Lys Glu Ile Asp Val Pro Glu Asn Leu Thr
165 170 175

Val Ala Glu Ile Lys Gln Arg Ala Ala Gln Ser Glu Val Ser Ile Val
180 185 190

Asn Gln Glu Arg Glu Gln Glu Ile Lys Asp Tyr Ile Asp Gln Ile Lys
195 200 205

Arg Asp Gly Asp Thr Ile Gly Gly Val Val Glu Thr Val Val Gly Gly
210 215 220

Val Pro Val Gly Leu Gly Ser Tyr Val Gln Trp Asp Arg Lys Leu Asp
225 230 235 240

Ala Arg Leu Ala Gln Ala Val Val Ser Ile Asn Ala Phe Lys Gly Val
245 250 255

Glu Phe Gly Leu Gly Phe Glu Ala Gly Tyr Arg Lys Gly Ser Gln Val
260 265 270

Met Asp Glu Ile Leu Trp Ser Lys Glu Asp Gly Tyr Thr Arg Arg Thr
275 280 285

Asn Asn Leu Gly Gly Phe Glu Gly Gly Met Thr Asn Gly Gln Pro Ile
290 295 300

Val Val Arg Gly Val Met Lys Pro Ile Pro Thr Leu Tyr Lys Pro Leu
305 310 315 320

Met Ser Val Asp Ile Glu Thr His Glu Pro Tyr Lys Ala Thr Val Glu
325 330 335

Arg Ser Asp Pro Thr Ala Leu Pro Ala Ala Gly Met Val Met Glu Ala
340 345 350

Val Val Ala Thr Val Leu Ala Gln Glu Ile Leu Glu Lys Phe Ser Ser
355 360 365

Asp Asn Leu Glu Glu Leu Lys Glu Ala Val Ala Lys His Arg Asp Tyr
370 375 380

Thr Lys Asn Tyr
385

<210> 201

<211> 390

<212> PRT

<213> Streptococcus pneumoniae

<400> 201

Met Val Val Met Asn Arg Ile Arg Val Ser Lys Arg Val Glu Lys Lys
1 5 10 15

Leu Ala Lys Gly Leu Val Leu Leu Glu Ala Ser Asp Leu Glu Asn Val
20 25 30

Asn Leu Lys Asp Gln Glu Val Glu Val Gln Gly Gln Glu Gly Asn Phe
35 40 45

Leu Gly Thr Ala Tyr Leu Ser Gln Gln Asn Lys Gly Leu Gly Trp Phe
50 55 60

Ile Ser Lys Asp Lys Val Ala Phe Asn Gln Ala Phe Phe Glu Thr Leu
65 70 75 80

Phe Arg Lys Ala Lys Glu Lys Arg Asn Ala Tyr Tyr Gln Asp Asp Leu
85 90 95

Thr Thr Ala Phe Arg Leu Phe Asn Gln Glu Gly Asp Gly Phe Gly Gly
100 105 110

Leu Thr Val Asp Leu Tyr Gly Asp Tyr Ala Val Phe Ser Trp Tyr Asn
115 120 125

Ser Tyr Val Tyr Gln Ile Arg Gln Thr Ile Ser Glu Ala Phe Arg Gln
130 135 140

Val Phe Pro Glu Val Leu Gly Ala Tyr Glu Lys Ile Arg Phe Lys Gly
145 150 155 160

Leu Asp Tyr Glu Ser Ala His Val Tyr Gly Gln Glu Ala Pro Asp Phe
165 170 175

Phe Asn Val Leu Glu Asn Gly Val Leu Tyr Gln Val Phe Met Asn Asp
180 185 190

Gly Leu Met Thr Gly Ile Phe Leu Asp Gln His Glu Val Arg Gly Ser
195 200 205

Leu Val Asp Gly Leu Ala Met Gly Lys Ser Leu Leu Asn Met Phe Ser
210 215 220

Tyr Thr Ala Ala Phe Ser Val Ala Ala Ala Met Gly Gly Ala Ser His
225 230 235 240

Thr Thr Ser Val Asp Leu Ala Lys Arg Ser Arg Glu Leu Ser Gln Ala
245 250 255

His Phe Gln Ala Asn Gly Leu Ser Thr Asp Glu His Arg Phe Ile Val
260 265 270

Met Asp Val Phe Glu Tyr Phe Lys Tyr Ala Lys Arg Lys Asp Leu Thr
275 280 285

Tyr Asp Val Ile Val Leu Asp Pro Pro Ser Phe Ala Arg Asn Lys Lys
290 295 300

Gln Thr Phe Ser Val Ala Lys Asp Tyr His Lys Leu Ile Ser Gln Ser
305 310 315 320

Leu Glu Ile Leu Asn Pro Gly Gly Ile Ile Ile Ala Ser Thr Asn Ala
325 330 335

Ala Asn Val Ser Arg Gln Lys Phe Thr Glu Gln Ile Asp Lys Gly Phe
340 345 350

Ala Gly Arg Ser Tyr Gln Ile Leu Asn Lys Tyr Gly Leu Pro Ala Asp
355 360 365

Phe Ala Tyr Asn Lys Lys Asp Glu Ser Ser Asn Tyr Leu Lys Val Ile
370 375 380

Ser Met Lys Val Ser Lys
385 390

<210> 202

<211> 428

<212> PRT

<213> Streptococcus pneumoniae

<400> 202

Met Thr Lys Thr Leu Lys Arg Pro Glu Val Leu Ser Pro Ala Gly Thr
1   5   10   15

Leu Glu Lys Leu Lys Val Ala Val Gln Tyr Gly Ala Asp Ala Val Phe
            20   25   30

Ile Gly Gly Gln Ala Tyr Gly Leu Arg Ser Arg Ala Gly Asn Phe Thr
        35   40   45

Phe Glu Gln Met Glu Glu Gly Val Gln Phe Ala Ala Lys Tyr Gly Ala
    50   55   60

Lys Val Tyr Val Ala Ala Asn Met Val Met His Glu Gly Asn Glu Ala
65   70   75   80

Gly Ala Gly Glu Trp Phe Arg Lys Leu Arg Asp Ile Gly Ile Ala Ala
                85   90   95

Val Ile Val Ser Asp Pro Ala Leu Ile Met Ile Ala Val Thr Glu Ala
            100   105   110

Pro Gly Leu Glu Ile His Leu Ser Thr Gln Ala Ser Ala Thr Asn Tyr
        115   120   125

Glu Thr Leu Glu Phe Trp Lys Glu Leu Gly Leu Thr Arg Val Val Leu
    130   135   140

Ala Arg Glu Val Ser Met Glu Glu Leu Ala Glu Ile Arg Lys Arg Thr
145   150   155   160

Asp Val Glu Ile Glu Ala Phe Val His Gly Ala Met Cys Ile Ser Tyr
                165   170   175

Ser Gly Arg Cys Thr Leu Ser Asn His Met Ser Met Arg Asp Ala Asn
            180   185   190

Arg Gly Gly Cys Ser Gln Ser Cys Arg Trp Lys Tyr Asp Leu Tyr Asp
        195   200   205

Met Pro Phe Gly Lys Glu Arg Lys Ser Leu Gln Gly Glu Ile Pro Glu
    210   215   220

Glu Phe Ser Met Ser Ala Val Asp Met Ser Met Ile Asp His Ile Pro
225   230   235   240

Asp Met Ile Glu Asn Gly Val Asp Ser Leu Lys Ile Glu Gly Arg Met
                245   250   255

Lys Ser Ile His Tyr Val Ser Thr Val Thr Asn Cys Tyr Lys Ala Ala
260 265 270

Val Asp Ala Tyr Leu Glu Ser Pro Glu Lys Phe Glu Ala Ile Lys Gln
275 280 285

Asp Leu Val Asp Glu Met Trp Lys Val Ala Gln Arg Glu Leu Ala Thr
290 295 300

Gly Phe Tyr Tyr Gly Thr Pro Ser Glu Asn Glu Gln Leu Phe Gly Ala
305 310 315 320

Arg Arg Lys Ile Pro Glu Tyr Lys Phe Val Ala Glu Val Val Ser Tyr
325 330 335

Asp Asp Ala Ala Gln Thr Ala Thr Ile Arg Gln Arg Asn Val Ile Asn
340 345 350

Glu Gly Asp Gln Val Glu Phe Tyr Gly Pro Gly Phe Arg His Phe Glu
355 360 365

Thr Tyr Ile Glu Asp Leu His Asp Ala Lys Gly Asn Lys Ile Asp Arg
370 375 380

Ala Pro Asn Pro Met Glu Leu Leu Thr Ile Lys Val Pro Gln Pro Val
385 390 395 400

Gln Ser Gly Asp Met Val Arg Ala Leu Lys Glu Gly Leu Ile Asn Leu
405 410 415

Tyr Lys Glu Asp Gly Thr Ser Val Thr Val Arg Ala
420 425

<210> 203

<211> 280

<212> PRT

<213> Streptococcus pneumoniae

<400> 203

Met Asn Thr Tyr Gln Leu Asn Asn Gly Val Glu Ile Pro Val Leu Gly
1 5 10 15

Phe Gly Thr Phe Lys Ala Lys Asp Gly Glu Glu Ala Tyr Arg Ala Val
20 25 30

Leu Glu Ala Leu Lys Ala Gly Tyr Arg His Ile Asp Thr Ala Ala Ile
35 40 45

Tyr Gln Asn Glu Glu Ser Val Gly Gln Ala Ile Lys Asp Ser Gly Val
50 55 60

Pro Arg Glu Glu Met Phe Val Thr Thr Lys Leu Trp Asn Ser Gln Gln
65 70 75 80

Thr Tyr Glu Gln Thr Arg Gln Ala Leu Glu Lys Ser Ile Glu Lys Leu
85 90 95

Gly Leu Asp Tyr Leu Asp Leu Tyr Leu Ile His Trp Pro Asn Pro Lys
100 105 110

Pro Leu Arg Glu Asn Asp Ala Trp Lys Thr Arg Asn Ala Glu Val Trp
115 120 125

Arg Ala Met Glu Asp Leu Tyr Gln Glu Gly Lys Ile Arg Ala Ile Gly
130 135 140

Val Ser Asn Phe Leu Pro His His Leu Asp Ala Leu Leu Glu Thr Ala
145 150 155 160

Thr Ile Val Pro Ala Val Asn Gln Val Arg Leu Ala Pro Gly Val Tyr
165 170 175

Gln Asp Gln Val Val Ala Tyr Cys Arg Glu Lys Gly Ile Leu Leu Glu
180 185 190

Ala Trp Gly Pro Phe Gly Gln Gly Glu Leu Phe Asp Ser Lys Gln Val
195 200 205

Gln Glu Ile Ala Ala Asn His Gly Lys Ser Val Ala Gln Ile Ala Leu
210 215 220

Ala Trp Ser Leu Ala Glu Gly Phe Leu Pro Leu Pro Lys Ser Val Thr
225 230 235 240

Thr Ser Arg Ile Gln Ala Asn Leu Asp Cys Phe Gly Ile Glu Leu Ser
245 250 255

His Glu Glu Arg Glu Thr Leu Lys Thr Ile Ala Val Gln Ser Gly Ala
260 265 270

Pro Arg Val Asp Asp Val Asp Phe
275 280

<210> 204

<211> 551

<212> PRT

<213> Streptococcus pneumoniae

<400> 204

Leu Ser Glu Lys Ser Arg Glu Glu Glu Lys Leu Ser Phe Lys Glu Gln
1 5 10 15

Ile Leu Arg Asp Leu Glu Lys Val Lys Gly Tyr Asp Glu Val Leu Lys
20 25 30

Glu Asp Glu Ala Val Val Arg Thr Pro Ala Asn Glu Pro Ser Thr Glu
35 40 45

Glu Leu Met Ala Asp Ser Leu Ser Thr Val Glu Glu Ile Met Arg Lys
50 55 60

Ala Pro Thr Val Pro Thr His Pro Ser Gln Gly Val Pro Ala Ser Pro
65 70 75 80

Ala Asp Glu Ile Gln Arg Glu Thr Pro Gly Val Pro Ser His Pro Ser
85 90 95

Gln Asp Val Pro Ser Ser Pro Ala Glu Glu Ser Gly Ser Arg Pro Gly
100 105 110

Pro Gly Pro Val Arg Pro Lys Lys Leu Glu Arg Glu Tyr Asn Glu Thr
115 120 125

Pro Thr Arg Val Ala Val Ser Tyr Thr Thr Ala Glu Lys Lys Ala Glu
130 135 140

Gln Ala Gly Pro Glu Thr Pro Thr Pro Ala Thr Glu Thr Val Asp Ile
145 150 155 160

Ile Arg Asp Thr Ser Arg Arg Ser Arg Arg Glu Gly Ala Lys Pro Val
165 170 175

Lys Pro Lys Lys Glu Lys Lys Ser His Val Lys Ala Phe Val Ile Ser
180 185 190

Phe Leu Val Phe Leu Ala Leu Leu Ser Ala Gly Gly Tyr Phe Gly Tyr
195 200 205

Gln Tyr Val Leu Asp Ser Leu Leu Pro Ile Asp Ala Asn Ser Lys Lys
210 215 220

Tyr Val Thr Val Gly Ile Pro Glu Gly Ser Asn Val Gln Glu Ile Gly
225 230 235 240

Thr Thr Leu Glu Lys Ala Gly Leu Val Lys His Gly Leu Ile Phe Ser
245 250 255

Phe Tyr Ala Lys Tyr Lys Asn Tyr Thr Asp Leu Lys Ala Gly Tyr Tyr
260 265 270

Asn Leu Gln Lys Ser Met Ser Thr Glu Asp Leu Leu Lys Glu Leu Gln
275 280 285

Lys Gly Gly Thr Asp Glu Pro Gln Glu Pro Val Leu Ala Thr Leu Thr
290 295 300

Ile Pro Glu Gly Tyr Thr Leu Asp Gln Ile Ala Gln Ala Val Gly Gln
305 310 315 320

Leu Gln Gly Asp Phe Lys Glu Ser Leu Thr Ala Glu Ala Phe Leu Ala
325 330 335

Lys Val Gln Asp Glu Thr Phe Ile Ser Gln Ala Val Ala Lys Tyr Pro
340 345 350

Thr Leu Leu Glu Ser Leu Pro Val Lys Asp Ser Gly Ala Arg Tyr Arg
355 360 365

Leu Glu Gly Tyr Leu Phe Pro Ala Thr Tyr Ser Ile Lys Glu Ser Thr
370 375 380

Thr Ile Glu Ser Leu Ile Asp Glu Met Leu Ala Ala Met Asp Lys Asn
385 390 395 400

Leu Ser Pro Tyr Tyr Ser Thr Ile Lys Ser Lys Asn Leu Thr Val Asn
405 410 415

Glu Leu Leu Thr Ile Ala Ser Leu Val Glu Lys Glu Gly Ala Lys Thr
420 425 430

Glu Asp Arg Lys Leu Ile Ala Gly Val Phe Tyr Asn Arg Leu Asn Arg
435 440 445

Asp Met Pro Leu Gln Ser Asn Ile Ala Ile Leu Tyr Ala Gln Gly Lys
450 455 460

Leu Gly Gln Asn Ile Ser Leu Ala Glu Asp Val Ala Ile Asp Thr Asn
465 470 475 480

Ile Asp Ser Pro Tyr Asn Val Tyr Lys Asn Val Gly Leu Met Pro Gly
485 490 495

Pro Val Asp Ser Pro Ser Leu Asp Ala Ile Glu Ser Ser Ile Asn Gln
500 505 510

Thr Lys Ser Asp Asn Leu Tyr Phe Val Ala Asp Val Thr Glu Gly Lys
515 520 525

Val Tyr Tyr Ala Asn Asn Gln Glu Asp His Asp Arg Asn Val Ala Glu
530 535 540

His Val Asn Ser Lys Leu Asn
545 550

<210> 205

<211> 205

<212> PRT

<213> Streptococcus pneumoniae

<400> 205

Met Lys Gln Glu Arg Phe Pro Leu Val Ser Asp Asp Glu Val Met Leu
1 5 10 15

Thr Glu Met Pro Val Met Asn Leu Tyr Asp Glu Ser Asp Leu Ile Ser
20 25 30

Asn Ile Lys Gly Glu Tyr Arg Asp Lys Asn Tyr Leu Glu Trp Ala Pro
35 40 45

Ile Ala Glu Glu Lys Pro Val Lys Pro Ile Glu Lys Gln Val Glu Lys
50 55 60

Pro Lys Lys Ala Pro Leu Gly Val Lys Lys Glu Gly Lys Ser Tyr Ala
65 70 75 80

Glu Val Ala Arg Glu Glu Ala Arg Ala Asp Leu Lys Lys Lys Arg Ser
85 90 95

Ala Asn Tyr Leu Thr Gln Asp Phe Ser Leu Ala Arg Arg His Ser Gln
100 105 110

Pro Ser Leu Val Arg Gln Gly Asn Gln Pro Thr Ala Pro Phe Gln Lys
115 120 125

Glu Asn Pro Gly Glu Phe Val Lys Tyr Ser Gln Lys Leu Thr Gln Ser
130 135 140

His Tyr Ile Leu Ala Glu Glu Val His Ser Ile Pro Thr Lys Asn Glu
145 150 155 160

Glu Val Ser Ala Pro Ala Pro Lys Lys Asn Asn Tyr Asp Phe Leu Lys
165 170 175

Lys Ser Gln Ile Tyr Asn Lys Lys Ser Lys Gln Thr Glu Gln Glu Arg
180 185 190

Arg Val Ala Gln Glu Leu Asn Leu Thr Arg Met Thr Glu
195 200 205

<210> 206

<211> 652

<212> PRT

<213> Streptococcus pneumoniae

<400> 206

Met Lys Lys Ser Lys Ser Lys Tyr Leu Thr Leu Ala Gly Leu Val Leu
1 5 10 15

Gly Thr Gly Val Leu Leu Ser Ala Cys Gly Asn Ser Ser Thr Ala Ser
20 25 30

Lys Thr Tyr Asn Tyr Val Tyr Ser Ser Asp Pro Ser Ser Leu Asn Tyr
35 40 45

Leu Ala Glu Asn Arg Ala Ala Thr Ser Asp Ile Val Ala Asn Leu Val
50 55 60

Asp Gly Leu Leu Glu Asn Asp Gln Tyr Gly Asn Ile Ile Pro Ser Leu
65 70 75 80

Ala Glu Asp Trp Thr Val Ser Gln Asp Gly Leu Thr Tyr Thr Tyr Lys
85 90 95

Leu Arg Lys Asp Ala Lys Trp Phe Thr Ser Glu Gly Glu Glu Tyr Ala
100 105 110

Pro Val Thr Ala Gln Asp Phe Val Thr Gly Leu Gln Tyr Ala Ala Asp
115 120 125

Lys Lys Ser Glu Ala Leu Tyr Leu Val Gln Asp Ser Val Ala Gly Leu
130 135 140

Asp Asp Tyr Ile Thr Gly Lys Thr Ser Asp Phe Ser Thr Val Gly Val
145 150 155 160

Lys Ala Leu Asp Asp Gln Thr Val Gln Tyr Thr Leu Val Lys Pro Glu
165 170 175

Leu Tyr Trp Asn Ser Lys Thr Leu Ala Thr Ile Leu Phe Pro Val Asn
180 185 190

Ala Asp Phe Leu Lys Ser Lys Gly Asp Asp Phe Gly Lys Ala Asp Pro
195 200 205

Ser Ser Ile Leu Tyr Asn Gly Pro Phe Leu Met Lys Ala Leu Val Ser
210 215 220

Lys Ser Ala Ile Glu Tyr Lys Lys Asn Pro Asn Tyr Trp Asp Ala Lys
225 230 235 240

Asn Val Phe Val Asp Asp Val Lys Leu Thr Tyr Tyr Asp Gly Ser Asp
245 250 255

Gln Glu Ser Leu Glu Arg Asn Phe Thr Ala Gly Ala Tyr Thr Thr Ala
260 265 270

Arg Leu Phe Pro Asn Ser Ser Ser Tyr Glu Gly Ile Lys Glu Lys Tyr
275 280 285

Lys Asn Asn Ile Ile Tyr Ser Met Gln Asn Ser Thr Ser Tyr Phe Phe
290 295 300

Asn Phe Asn Leu Asp Arg Lys Ser Tyr Asn Tyr Thr Ser Lys Thr Ser
305 310 315 320

Asp Ile Glu Lys Lys Ser Thr Gln Glu Ala Val Leu Asn Lys Asn Phe
325 330 335

Arg Gln Ala Ile Asn Phe Ala Phe Asp Arg Thr Ser Tyr Gly Ala Gln
340 345 350

Ser Glu Gly Lys Glu Gly Ala Thr Lys Ile Leu Arg Asn Leu Val Val
355 360 365

Pro Pro Asn Phe Val Ser Ile Lys Gly Lys Asp Phe Gly Glu Val Val
370 375 380

Ala Ser Lys Met Val Asn Tyr Gly Lys Glu Trp Gln Gly Ile Asn Phe
385 390 395 400

Ala Asp Gly Gln Asp Pro Tyr Tyr Asn Pro Glu Lys Ala Lys Ala Lys
405 410 415

Phe Ala Glu Ala Lys Lys Glu Leu Glu Ala Lys Gly Val Gln Phe Pro
420 425 430

Ile His Leu Asp Lys Thr Val Glu Val Thr Asp Lys Val Gly Ile Gln
435 440 445

Gly Val Ser Ser Ile Lys Gln Ser Ile Glu Ser Val Leu Gly Ser Asp
450 455 460

Asn Val Val Ile Asp Ile Gln Gln Leu Thr Ser Asp Glu Phe Asp Ser
465 470 475 480

Ser Gly Tyr Phe Ala Gln Thr Ala Ala Gln Lys Asp Tyr Asp Leu Tyr
485 490 495

His Gly Gly Trp Gly Pro Asp Tyr Gln Asp Pro Ser Thr Tyr Leu Asp
500 505 510

Ile Phe Asn Thr Asn Ser Gly Gly Phe Leu Gln Asn Leu Gly Leu Glu
515 520 525

Pro Gly Glu Ala Asn Asp Lys Ala Lys Ala Val Gly Leu Asp Val Tyr
530 535 540

Thr Gln Met Leu Glu Glu Ala Asn Lys Glu Gln Asp Pro Ala Lys Arg
545 550 555 560

Tyr Glu Lys Tyr Ala Asp Ile Gln Ala Trp Leu Ile Asp Ser Ser Leu
565 570 575

Val Leu Pro Ser Val Ser Arg Gly Gly Thr Pro Ser Leu Arg Arg Thr
580 585 590

Val Pro Phe Ala Ala Ala Tyr Gly Leu Thr Gly Thr Lys Gly Val Glu
595 600 605

Ser Tyr Lys Tyr Leu Lys Val Gln Asp Lys Ile Val Thr Thr Asp Glu
610 615 620

Tyr Ala Lys Ala Arg Glu Lys Trp Leu Lys Glu Lys Glu Glu Ser Asn
625 630 635 640

Lys Lys Ala Gln Glu Glu Leu Ala Lys His Val Lys
645 650

<210> 207

<211> 506

<212> PRT

<213> Streptococcus pneumoniae

<400> 207

Val Glu Gln His Ser Asp Val Cys Tyr Ile Phe Tyr Arg Arg Glu Arg
1 5 10 15

Leu Lys Thr Lys Ile Gly Leu Ala Ser Ile Cys Leu Leu Gly Leu Ala
20 25 30

Thr Ser His Val Ala Ala Asn Glu Thr Glu Val Ala Lys Thr Ser Gln
35 40 45

Asp Thr Thr Thr Ala Ser Ser Ser Ser Glu Gln Asn Gln Ser Ser Asn
50 55 60

Lys Thr Gln Thr Ser Ala Glu Val Gln Thr Asn Ala Ala Ala His Trp
65 70 75 80

Asp Gly Asp Tyr Tyr Val Lys Asp Asp Gly Ser Lys Ala Gln Ser Glu
85 90 95

Trp Ile Phe Asp Asn Tyr Tyr Lys Ala Trp Phe Tyr Ile Asn Ser Asp
100 105 110

Gly Arg Tyr Ser Gln Asn Glu Trp His Gly Asn Tyr Tyr Leu Lys Ser
115 120 125

Gly Gly Tyr Met Ala Gln Asn Glu Trp Ile Tyr Asp Ser Asn Tyr Lys
130 135 140

Ser Trp Phe Tyr Leu Lys Ser Asp Gly Ala Tyr Ala His Gln Glu Trp
145 150 155 160

Gln Leu Ile Gly Asn Lys Trp Tyr Tyr Phe Lys Lys Trp Gly Tyr Met
165 170 175

Ala Lys Ser Gln Trp Gln Gly Ser Tyr Phe Leu Asn Gly Gln Gly Ala
180 185 190

Met Met Gln Asn Glu Trp Leu Tyr Asp Pro Ala Tyr Ser Ala Tyr Phe
195 200 205

Tyr Leu Lys Ser Asp Gly Thr Tyr Ala Asn Gln Glu Trp Gln Lys Val
210 215 220

Gly Gly Lys Trp Tyr Tyr Phe Lys Lys Trp Gly Tyr Met Ala Arg Asn
225 230 235 240

Glu Trp Gln Gly Asn Tyr Tyr Leu Thr Gly Ser Gly Ala Met Ala Thr
245 250 255

Asp Glu Val Ile Met Asp Gly Thr Arg Tyr Ile Phe Ala Ala Ser Gly
260 265 270

Glu Leu Lys Glu Lys Lys Asp Leu Asn Val Gly Trp Val His Arg Asp
275 280 285

Gly Lys Arg Tyr Phe Phe Asn Asn Arg Glu Glu Gln Val Gly Thr Glu
290 295 300

His Ala Lys Lys Val Ile Asp Ile Ser Glu His Asn Gly Arg Ile Asn
305 310 315 320

Asp Trp Lys Lys Val Ile Asp Glu Asn Glu Val Asp Gly Val Ile Val
325 330 335

Arg Leu Gly Tyr Ser Gly Lys Glu Asp Lys Glu Leu Ala His Asn Ile
340 345 350

Lys Glu Leu Asn Arg Leu Gly Ile Pro Tyr Gly Val Tyr Leu Tyr Thr
355 360 365

Tyr Ala Glu Asn Glu Thr Asp Ala Glu Ser Asp Ala Lys Gln Thr Ile
370 375 380

Glu Leu Ile Lys Lys Tyr Asn Met Asn Leu Ser Tyr Pro Ile Tyr Tyr
385 390 395 400

Asp Val Glu Asn Trp Glu Tyr Val Asn Lys Ser Lys Arg Ala Pro Ser
405 410 415

Asp Thr Gly Thr Trp Val Lys Ile Ile Asn Lys Tyr Met Asp Thr Met
420 425 430

Lys Gln Ala Gly Tyr Gln Asn Val Tyr Val Tyr Ser Tyr Arg Ser Leu
435 440 445

Leu Gln Thr Arg Leu Lys His Pro Asp Ile Leu Lys His Val Asn Trp
450 455 460

Val Ala Ala Tyr Thr Asn Ala Leu Glu Trp Glu Asn Pro His Tyr Ser
465 470 475 480

Gly Lys Lys Gly Trp Gln Tyr Thr Ser Ser Glu Tyr Met Lys Gly Ile
485 490 495

Gln Gly Arg Val Asp Val Ser Val Trp Tyr
500 505

<210> 208

<211> 158

<212> PRT

<213> Streptococcus pneumoniae

<400> 208

Met Ala Lys Glu Pro Trp Gln Glu Asp Ile Tyr Asp Gln Glu Glu Ser
1 5 10 15

Arg Ala Glu Arg Arg His Arg Asn His Gly Gly Ala Asp Arg Met Ala
20 25 30

Asn Arg Ile Leu Thr Ile Leu Ala Ser Ile Phe Phe Val Ile Val Val
35 40 45

Val Met Val Ile Val Leu Ile Tyr Leu Ser Ser Gly Gly Ser Asn Arg
50 55 60

Thr Ala Ala Leu Lys Gly Phe His Asp Ser Asp Ala Ser Val Val Gln
65 70 75 80

Ile Ser Ser Ser Ser Ser Ser Gln Pro Glu Gln Ser Ser Glu Pro Glu
85 90 95

Ser Thr Ser Ser Ser Ser Glu Glu Ala Ala Asn Pro Glu Gly Thr Ile
100 105 110

Lys Val Leu Ala Gly Glu Gly Glu Ala Ala Ile Ala Ala Arg Ala Gly
115 120 125

Ile Ser Ile Ala Gln Leu Glu Ala Leu Asn Pro Gly His Met Ala Thr
130 135 140

Gly Ser Trp Phe Ala Asn Pro Gly Asp Val Ile Lys Ile Lys
145 150 155

<210> 209

<211> 262

<212> PRT

<213> Streptococcus pneumoniae

<400> 209

Met Pro Ile Thr Ser Leu Glu Ile Lys Asp Lys Thr Phe Gly Thr Arg
1 5 10 15

Phe Arg Gly Phe Asp Pro Glu Glu Val Asp Glu Phe Leu Asp Ile Val
20 25 30

Val Arg Asp Tyr Glu Asp Leu Val Arg Ala Asn His Asp Lys Asn Leu
35 40 45

Arg Ile Lys Ser Leu Glu Glu Arg Leu Ser Tyr Phe Asp Glu Ile Lys
50 55 60

Asp Ser Leu Ser Gln Ser Val Leu Ile Ala Gln Asp Thr Ala Glu Arg
65 70 75 80

Val Lys Gln Ala Ala His Glu Arg Ser Asn Asn Ile Ile His Gln Ala
85 90 95

Glu Gln Asp Ala Gln Arg Leu Leu Glu Glu Ala Lys Tyr Lys Ala Asn
100 105 110

Glu Ile Leu Arg Gln Ala Thr Asp Asn Ala Lys Lys Val Ala Val Glu
115 120 125

Thr Glu Glu Leu Lys Asn Lys Ser Arg Val Phe His Gln Arg Leu Lys
130 135 140

Ser Thr Ile Glu Ser Gln Leu Ala Ile Val Glu Ser Ser Asp Trp Glu
145 150 155 160

Asp Ile Leu Arg Pro Thr Ala Thr Tyr Leu Gln Thr Ser Asp Glu Ala
165 170 175

Phe Lys Glu Val Val Ser Glu Val Leu Gly Glu Pro Ile Pro Ala Pro
180 185 190

Ile Glu Glu Glu Pro Ile Asp Met Thr Arg Gln Phe Ser Gln Ala Glu
195 200 205

Met Ala Glu Leu Gln Ala Arg Ile Glu Val Ala Asp Lys Glu Leu Ser
210 215 220

Glu Phe Glu Ala Gln Ile Lys Gln Glu Val Glu Ala Pro Thr Pro Val
225 230 235 240

Val Ser Pro Gln Val Glu Glu Glu Pro Leu Leu Ile Gln Leu Ala Gln
245 250 255

Cys Met Lys Asn Gln Lys
260

<210> 210

<211> 179

<212> PRT

<213> Streptococcus pneumoniae

<400> 210

Met Ser Leu Lys Asp Arg Phe Asp Arg Phe Ile Asp Tyr Phe Thr Glu
1 5 10 15

Asp Glu Asp Ser Ser Leu Pro Tyr Glu Lys Arg Asp Glu Pro Val Phe
20 25 30

Thr Ser Val Asn Ser Ser Gln Glu Pro Ala Leu Pro Met Asn Gln Pro
35 40 45

Ser Gln Ser Ala Gly Thr Lys Glu Asn Asn Ile Thr Arg Leu His Ala
50 55 60

Arg Gln Gln Glu Leu Ala Asn Gln Ser Gln Arg Ala Thr Asp Lys Val
65 70 75 80

Ile Ile Asp Val Arg Tyr Pro Arg Lys Tyr Glu Asp Ala Thr Glu Ile
85 90 95

Val Asp Leu Leu Ala Gly Asn Glu Ser Ile Leu Ile Asp Phe Gln Tyr
100 105 110

Met Thr Glu Val Gln Ala Arg Arg Cys Leu Asp Tyr Leu Asp Gly Ala
115 120 125

Cys His Val Leu Ala Gly Asn Leu Lys Lys Val Ala Ser Thr Met Tyr
130 135 140

Leu Leu Thr Pro Val Asn Val Ile Val Asn Val Glu Asp Ile Arg Leu
145 150 155 160

Pro Asp Glu Asp Gln Gln Gly Glu Phe Gly Phe Asp Met Lys Arg Asn
165 170 175

Arg Val Arg

<210> 211

<211> 305

<212> PRT

<213> Streptococcus pneumoniae

<400> 211

Met Ser Asp Leu Lys Lys Tyr Glu Gly Val Ile Pro Ala Phe Tyr Ala
1 5 10 15

Cys Tyr Asp Asp Gln Gly Glu Val Ser Pro Glu Arg Thr Arg Ala Leu
20 25 30

Val Gln Tyr Phe Ile Asp Lys Gly Val Gln Gly Leu Tyr Val Asn Gly
35 40 45

Ser Ser Gly Glu Cys Ile Tyr Gln Ser Val Glu Asp Arg Lys Leu Ile
50 55 60

Leu Glu Glu Val Met Ala Val Ala Lys Gly Lys Leu Thr Ile Ile Ala
65 70 75 80

His Val Ala Cys Asn Asn Thr Lys Asp Ser Met Glu Leu Ala Arg His
85 90 95

Ala Glu Ser Leu Gly Val Asp Ala Ile Ala Thr Ile Pro Pro Ile Tyr
100 105 110

Phe Arg Leu Pro Glu Tyr Ser Val Ala Lys Tyr Trp Asn Asp Ile Ser
115 120 125

Ser Ala Ala Pro Asn Thr Asp Tyr Val Ile Tyr Asn Ile Pro Gln Leu
130 135 140

Ala Gly Val Ala Leu Thr Pro Ser Leu Tyr Thr Glu Met Leu Lys Asn
145 150 155 160

Pro Arg Val Ile Gly Val Lys Asn Ser Ser Met Pro Val Gln Asp Ile
165 170 175

Gln Thr Phe Val Ser Leu Gly Gly Glu Asp His Ile Val Phe Asn Gly
180 185 190

Pro Asp Glu Gln Phe Leu Gly Gly Arg Leu Met Gly Ala Arg Ala Gly
195 200 205

Ile Gly Gly Thr Tyr Gly Ala Met Pro Glu Leu Phe Leu Lys Leu Asn
210 215 220

Gln Leu Ile Ala Asp Lys Asp Leu Glu Thr Ala Arg Glu Leu Gln Tyr
225 230 235 240

Ala Ile Asn Ala Ile Ile Gly Lys Leu Thr Ser Ala His Gly Asn Met
245 250 255

Tyr Gly Val Ile Lys Glu Val Leu Lys Ile Asn Glu Gly Leu Asn Ile
260 265 270

Gly Ser Val Arg Ser Pro Leu Thr Pro Val Thr Glu Glu Asp Arg Pro
275 280 285

Val Val Glu Ala Ala Ala Ala Leu Ile Arg Glu Thr Lys Glu Arg Phe
290 295 300

Leu
305

<210> 212

<211> 697

<212> PRT

<213> Streptococcus pneumoniae

<400> 212

Met Asn Lys Arg Gly Leu Tyr Ser Lys Leu Gly Ile Ser Val Val Gly
1 5 10 15

Ile Ser Leu Leu Met Gly Val Pro Thr Leu Ile His Ala Asn Glu Leu
20 25 30

Asn Tyr Gly Gln Leu Ser Ile Ser Pro Ile Phe Gln Gly Gly Ser Tyr
35 40 45

Gln Leu Asn Asn Lys Ser Ile Asp Ile Ser Ser Leu Leu Leu Asp Lys
50 55 60

Leu Ser Gly Glu Ser Gln Thr Val Val Met Lys Phe Lys Ala Asp Lys
65 70 75 80

Pro Asn Ser Leu Gln Ala Leu Phe Gly Leu Ser Asn Ser Lys Ala Gly
85 90 95

Phe Lys Asn Asn Tyr Phe Ser Ile Phe Met Arg Asp Ser Gly Glu Ile
100 105 110

Gly Val Glu Ile Arg Asp Ala Gln Lys Gly Ile Asn Tyr Leu Phe Ser
115 120 125

Arg Pro Ala Ser Leu Trp Gly Lys His Lys Gly Gln Ala Val Glu Asn
130 135 140

Thr Leu Val Phe Val Ser Asp Ser Lys Asp Lys Thr Tyr Thr Met Tyr
145 150 155 160

Val Asn Gly Ile Glu Val Phe Ser Glu Thr Val Asp Thr Phe Leu Pro
165 170 175

Ile Ser Asn Ile Asn Gly Ile Asp Lys Ala Thr Leu Gly Ala Val Asn
180 185 190

Arg Glu Gly Lys Glu His Tyr Leu Ala Lys Gly Ser Ile Asp Glu Ile
195 200 205

Ser Leu Phe Asn Lys Ala Ile Ser Asp Gln Glu Val Ser Thr Ile Pro
210 215 220

Leu Ser Asn Pro Phe Gln Leu Ile Phe Gln Ser Gly Asp Ser Thr Gln
225 230 235 240

Ala Asn Tyr Phe Arg Ile Pro Thr Leu Tyr Thr Leu Ser Ser Gly Arg
245 250 255

Val Leu Ser Ser Ile Asp Ala Arg Tyr Gly Gly Thr His Asp Ser Lys
260 265 270

Ser Lys Ile Asn Ile Ala Thr Ser Tyr Ser Asp Asp Asn Gly Lys Thr
275 280 285

Trp Ser Glu Pro Ile Phe Ala Met Lys Phe Asn Asp Tyr Glu Glu Gln
290 295 300

Leu Val Tyr Trp Pro Arg Asp Asn Lys Leu Lys Asn Ser Gln Ile Ser
305 310 315 320

Gly Ser Ala Ser Phe Ile Asp Ser Ser Ile Val Glu Asp Lys Lys Ser
325 330 335

Gly Lys Thr Ile Leu Leu Ala Asp Val Met Pro Ala Gly Ile Gly Asn
340 345 350

Asn Asn Ala Asn Lys Ala Asp Ser Gly Phe Lys Glu Ile Asn Gly His
355 360 365

Tyr Tyr Leu Lys Leu Lys Lys Asn Gly Asp Asn Asp Phe Arg Tyr Thr
370 375 380

Val Arg Glu Asn Gly Val Val Tyr Asn Glu Thr Thr Asn Lys Pro Thr
385 390 395 400

Asn Tyr Thr Ile Asn Asp Lys Tyr Glu Val Leu Glu Gly Gly Lys Ser
405 410 415

Leu Thr Val Glu Gln Tyr Ser Val Asp Phe Asp Ser Gly Ser Leu Arg
420 425 430

Glu Arg His Asn Gly Lys Gln Val Pro Met Asn Val Phe Tyr Lys Asp
435 440 445

Ser Leu Phe Lys Val Thr Pro Thr Asn Tyr Ile Ala Met Thr Thr Ser
450 455 460

Gln Asn Arg Gly Glu Ser Trp Glu Gln Phe Lys Leu Leu Pro Pro Phe
465 470 475 480

Leu Gly Glu Lys His Asn Gly Thr Tyr Leu Cys Pro Gly Gln Gly Leu
485 490 495

Ala Leu Lys Ser Ser Asn Arg Leu Ile Phe Ala Thr Tyr Thr Ser Gly
500 505 510

Glu Leu Thr Tyr Leu Ile Ser Asp Asp Ser Gly Gln Thr Trp Lys Lys
515 520 525

Ser Ser Ala Ser Ile Pro Phe Lys Asn Ala Thr Ala Glu Ala Gln Met
530 535 540

Val Glu Leu Arg Asp Gly Val Ile Arg Thr Phe Phe Arg Thr Thr Thr
545 550 555 560

Gly Lys Ile Ala Tyr Met Thr Ser Arg Asp Ser Gly Glu Thr Trp Ser
565 570 575

Lys Val Ser Tyr Ile Asp Gly Ile Gln Gln Thr Ser Tyr Gly Thr Gln
580 585 590

Val Ser Ala Ile Lys Tyr Ser Gln Leu Ile Asp Gly Lys Glu Ala Val
595 600 605

Ile Leu Ser Thr Pro Asn Ser Arg Ser Gly Arg Lys Gly Gly Gln Leu
610 615 620

Val Val Gly Leu Val Asn Lys Glu Asp Asp Ser Ile Asp Trp Lys Tyr
625 630 635 640

His Tyr Asp Ile Asp Leu Pro Ser Tyr Gly Tyr Ala Tyr Ser Ala Ile
645 650 655

Thr Glu Leu Pro Asn His His Ile Gly Val Leu Phe Glu Lys Tyr Asp
660 665 670

Ser Trp Ser Arg Asn Glu Leu His Leu Ser Asn Val Val Gln Tyr Ile
675 680 685

Asp Leu Glu Ile Asn Asp Leu Thr Lys
690 695

<210> 213

<211> 946

<212> PRT

<213> Streptococcus pneumoniae

<400> 213

Met Asn Arg Ser Val Gln Glu Arg Lys Cys Arg Tyr Ser Ile Arg Lys
1 5 10 15

Leu Ser Val Gly Ala Val Ser Met Ile Val Gly Ala Val Val Phe Gly
20 25 30

Thr Ser Pro Val Leu Ala Gln Glu Gly Ala Ser Glu Gln Pro Leu Ala
35 40 45

Asn Glu Thr Gln Leu Ser Gly Glu Ser Ser Thr Leu Thr Asp Thr Glu
50 55 60

Lys Ser Gln Pro Ser Ser Glu Thr Glu Leu Ser Gly Asn Lys Gln Glu
65 70 75 80

Gln Glu Arg Lys Asp Lys Gln Glu Glu Lys Ile Pro Arg Asp Tyr Tyr
85 90 95

Ala Arg Asp Leu Glu Asn Val Glu Thr Val Ile Glu Lys Glu Asp Val
100 105 110

Glu Thr Asn Ala Ser Asn Gly Gln Arg Val Asp Leu Ser Ser Glu Leu
115 120 125

Asp Lys Leu Lys Lys Leu Glu Asn Ala Thr Val His Met Glu Phe Lys
130 135 140

Pro Asp Ala Lys Ala Pro Ala Phe Tyr Asn Leu Phe Ser Val Ser Ser
145 150 155 160

Ala Thr Lys Lys Asp Glu Tyr Phe Thr Met Ala Val Tyr Asn Asn Thr
165 170 175

Ala Thr Leu Glu Gly Arg Gly Ser Asp Gly Lys Gln Phe Tyr Asn Asn
180 185 190

Tyr Asn Asp Ala Pro Leu Lys Val Lys Pro Gly Gln Trp Asn Ser Val
195 200 205

Thr Phe Thr Val Glu Lys Pro Thr Ala Glu Leu Pro Lys Gly Arg Val
210 215 220

Arg Leu Tyr Val Asn Gly Val Leu Ser Arg Thr Ser Leu Arg Ser Gly
225 230 235 240

Asn Phe Ile Lys Asp Met Pro Asp Val Thr His Val Gln Ile Gly Ala
245 250 255

Thr Lys Arg Ala Asn Asn Thr Val Trp Gly Ser Asn Leu Gln Ile Arg
260 265 270

Asn Leu Thr Val Tyr Asn Arg Ala Leu Thr Pro Glu Glu Val Gln Lys
275 280 285

Arg Ser Gln Leu Phe Lys Arg Ser Asp Leu Glu Lys Lys Leu Pro Glu
290 295 300

Gly Ala Ala Leu Thr Glu Lys Thr Asp Ile Phe Glu Ser Gly Arg Asn
305 310 315 320

Gly Asn Pro Asn Lys Asp Gly Ile Lys Ser Tyr Arg Ile Pro Ala Leu
325 330 335

Leu Lys Thr Asp Lys Gly Thr Leu Ile Ala Gly Ala Asp Glu Arg Arg
340 345 350

Leu His Ser Ser Asp Trp Gly Asp Ile Gly Met Val Ile Arg Arg Ser
355 360 365

Glu Asp Asn Gly Lys Thr Trp Gly Asp Arg Val Thr Ile Thr Asn Leu
370 375 380

Arg Asp Asn Pro Lys Ala Ser Asp Pro Ser Ile Gly Ser Pro Val Asn
385 390 395 400

Ile Asp Met Val Leu Val Gln Asp Pro Glu Thr Lys Arg Ile Phe Ser
405 410 415

Ile Tyr Asp Met Phe Pro Glu Gly Lys Gly Ile Phe Gly Met Ser Ser
420 425 430

Gln Lys Glu Glu Ala Tyr Lys Lys Ile Asp Gly Lys Thr Tyr Gln Ile
435 440 445

Leu Tyr Arg Glu Gly Glu Lys Gly Ala Tyr Thr Ile Arg Glu Asn Gly
450 455 460

Thr Val Tyr Thr Pro Asp Gly Lys Ala Thr Asp Tyr Arg Val Val Val
465 470 475 480

Asp Pro Val Lys Pro Ala Tyr Ser Asp Lys Gly Asp Leu Tyr Lys Gly
485 490 495

Asp Gln Leu Leu Gly Asn Ile Tyr Phe Thr Thr Asn Lys Thr Ser Pro
500 505 510

Phe Arg Ile Ala Lys Asp Ser Tyr Leu Trp Met Ser Tyr Ser Asp Asp
515 520 525

Asp Gly Lys Thr Trp Ser Ala Pro Gln Asp Ile Thr Pro Met Val Lys
530 535 540

Ala Asp Trp Met Lys Phe Leu Gly Val Gly Pro Gly Thr Gly Ile Val
545 550 555 560

Leu Arg Asn Gly Pro His Lys Gly Arg Ile Leu Ile Pro Val Tyr Thr
565 570 575

Thr Asn Asn Val Ser His Leu Asp Gly Ser Gln Ser Ser Arg Val Ile
580 585 590

Tyr Ser Asp Asp His Gly Lys Thr Trp His Ala Gly Glu Ala Val Asn
595 600 605

Asp Asn Arg Gln Val Asp Gly Gln Lys Ile His Ser Ser Thr Met Asn
610 615 620

Asn Arg Arg Ala Gln Asn Thr Glu Ser Thr Val Val Gln Leu Asn Asn
625 630 635 640

Gly Asp Val Lys Leu Phe Met Arg Gly Leu Thr Gly Asp Leu Gln Val
645 650 655

Ala Thr Ser Lys Asp Gly Gly Val Thr Trp Glu Lys Asp Ile Lys Arg
660 665 670

Tyr Pro Gln Val Lys Asp Val Tyr Val Gln Met Ser Ala Ile His Thr
675 680 685

Met His Glu Gly Lys Glu Tyr Ile Ile Leu Ser Asn Ala Gly Gly Pro
690 695 700

Lys Arg Glu Asn Gly Met Val His Leu Ala Arg Val Glu Glu Asn Gly
705 710 715 720

Glu Leu Thr Trp Leu Lys His Asn Pro Ile Gln Lys Gly Glu Phe Ala
725 730 735

Tyr Asn Ser Leu Gln Glu Leu Gly Asn Gly Glu Tyr Gly Ile Leu Tyr
740 745 750

Glu His Thr Glu Lys Gly Gln Asn Ala Tyr Thr Leu Ser Phe Arg Lys
755 760 765

Phe Asn Trp Glu Phe Leu Ser Lys Asn Leu Ile Ser Pro Thr Glu Ala
770 775 780

Asn Arg Asp Gly Gln Arg Arg Asp Gly Gln Arg Ser Tyr Trp Leu Gly
785 790 795 800

Val Arg Leu Arg Ser Ile Gly Gln Gln Gly Ser Asn Pro Ser Ile Gly
805 810 815

Lys Trp Asn Ser Asp Phe Pro Asn Pro Val Gln Asp Leu Val Val Cys
820 825 830

Ser Arg Gly Arg Tyr Arg Thr Gly Asn Tyr Trp Tyr Ser Arg Lys His
835 840 845

Arg Lys Tyr Ala Ser Ser Cys Lys Ser Ser Arg Cys Gln Ser Ser Trp
850 855 860

Arg Ser Lys Trp Gln Ser Ser Gly Ala Ser Ser Arg Ile Tyr Arg Gly
865 870 875 880

Ser Trp Tyr Arg Ala Ser Cys Ser Asn Arg Arg Val Gly Ile Phe Ala
885 890 895

Cys Asn Ser Tyr Tyr Lys Lys Arg Leu Tyr Leu Gln Ser Ser Ser Cys
900 905 910

Ser Ala Gly Thr Ser Asn Arg Lys Gln Gly Glu Pro Pro Ser Phe Thr
915 920 925

Arg Thr Asn Ser Phe Leu Pro Trp Ser Val Tyr Ala Arg Glu Lys Glu
930 935 940

Arg Thr
945

<210> 214

<211> 659

<212> PRT

<213> Streptococcus pneumoniae

<400> 214

Met Ile Gln Ile Gly Lys Ile Phe Ala Gly Arg Tyr Arg Ile Val Lys
1 5 10 15

Gln Ile Gly Arg Gly Gly Met Ala Asp Val Tyr Leu Ala Lys Asp Leu
20 25 30

Ile Leu Asp Gly Glu Glu Val Ala Val Lys Val Leu Arg Thr Asn Tyr
35 40 45

Gln Thr Asp Pro Ile Ala Val Ala Arg Phe Gln Arg Glu Ala Arg Ala
50 55 60

Met Ala Asp Leu Asp His Pro His Ile Val Arg Ile Thr Asp Ile Gly
65 70 75 80

Glu Glu Asp Gly Gln Gln Tyr Leu Ala Met Glu Tyr Val Ala Gly Leu
85 90 95

Asp Leu Lys Arg Tyr Ile Lys Glu His Tyr Pro Leu Ser Asn Glu Glu
100 105 110

Ala Val Arg Ile Met Gly Gln Ile Leu Leu Ala Met Arg Leu Ala His
115 120 125

Thr Arg Gly Ile Val His Arg Asp Leu Lys Pro Gln Asn Ile Leu Leu
130 135 140

Thr Pro Asp Gly Thr Ala Lys Val Thr Asp Phe Gly Ile Ala Val Ala
145 150 155 160

Phe Ala Glu Thr Ser Leu Thr Gln Thr Asn Ser Met Leu Gly Ser Val
165 170 175

His Tyr Leu Ser Pro Glu Gln Ala Arg Gly Ser Lys Ala Thr Val Gln
180 185 190

Ser Asp Ile Tyr Ala Met Gly Ile Ile Phe Tyr Glu Met Leu Thr Gly
195 200 205

His Ile Pro Tyr Asp Gly Asp Ser Ala Val Thr Ile Ala Leu Gln His
210 215 220

Phe Gln Lys Pro Leu Pro Ser Val Ile Ala Glu Asn Pro Ser Val Pro
225 230 235 240

Gln Ala Leu Glu Asn Val Ile Ile Lys Ala Thr Ala Lys Lys Leu Thr
245 250 255

Asn Arg Tyr Arg Ser Val Ser Glu Met Tyr Val Asp Leu Ser Ser Ser
260 265 270

Leu Ser Tyr Asn Arg Arg Asn Glu Ser Lys Leu Ile Phe Asp Glu Thr
275 280 285

Ser Lys Ala Asp Thr Lys Thr Leu Pro Lys Val Ser Gln Ser Thr Leu
290 295 300

Thr Ser Ile Pro Lys Val Gln Ala Gln Thr Glu His Lys Ser Ile Lys
305 310 315 320

Asn Pro Ser Gln Ala Val Thr Glu Glu Thr Tyr Gln Pro Gln Ala Pro
325 330 335

Lys Lys His Arg Phe Lys Met Arg Tyr Leu Ile Leu Leu Ala Ser Leu
340 345 350

Val Leu Val Ala Ala Ser Leu Ile Trp Ile Leu Ser Arg Thr Pro Ala
355 360 365

Thr Ile Ala Ile Pro Asp Val Ala Gly Gln Thr Val Ala Glu Ala Lys
370 375 380

Ala Thr Leu Lys Lys Ala Asn Phe Glu Ile Gly Glu Glu Lys Thr Glu
385 390 395 400

Ala Ser Glu Lys Val Glu Glu Gly Arg Ile Ile Arg Thr Asp Pro Gly
405 410 415

Ala Gly Thr Gly Arg Lys Glu Gly Thr Lys Ile Asn Leu Val Val Ser
420 425 430

Ser Gly Lys Gln Ser Phe Gln Ile Ser Asn Tyr Val Gly Arg Lys Ser
435 440 445

Ser Asp Val Ile Ala Glu Leu Lys Glu Lys Lys Val Pro Asp Asn Leu
450 455 460

Ile Lys Ile Glu Glu Glu Glu Ser Asn Glu Ser Glu Ala Gly Thr Val
465 470 475 480

Leu Lys Gln Ser Leu Pro Glu Gly Thr Thr Tyr Asp Leu Ser Lys Ala
485 490 495

Thr Gln Ile Val Leu Thr Val Ala Lys Lys Ala Thr Thr Ile Gln Leu
500 505 510

Gly Asn Tyr Ile Gly Arg Asn Ser Thr Glu Val Ile Ser Glu Leu Lys
515 520 525

Gln Lys Lys Val Pro Glu Asn Leu Ile Lys Ile Glu Glu Glu Glu Ser
530 535 540

Ser Glu Ser Glu Pro Gly Thr Ile Met Lys Gln Ser Pro Gly Ala Gly
545 550 555 560

Thr Thr Tyr Asp Val Ser Lys Pro Thr Gln Ile Val Leu Thr Val Ala
565 570 575

Lys Lys Val Thr Ser Val Ala Met Pro Ser Tyr Ile Gly Ser Ser Leu
580 585 590

Glu Phe Thr Lys Asn Asn Leu Ile Gln Ile Val Gly Ile Lys Glu Ala
595 600 605

Asn Ile Glu Val Val Glu Val Thr Thr Ala Pro Ala Gly Ser Ala Glu
610 615 620

Gly Met Val Val Glu Gln Ser Pro Arg Ala Gly Glu Lys Val Asp Leu
625 630 635 640

Asn Lys Thr Arg Val Lys Ile Ser Ile Tyr Lys Pro Lys Thr Thr Ser
645 650 655

Ala Thr Pro

<210> 215

<211> 311

<212> PRT

<213> Streptococcus pneumoniae

<400> 215

Met Thr Lys Leu Ile Phe Met Gly Thr Pro Asp Phe Ser Ala Thr Val
1 5 10 15

Leu Lys Gly Leu Leu Thr Asp Asp Arg Tyr Glu Ile Leu Ala Val Val
20 25 30

Thr Gln Pro Asp Arg Ala Val Gly Arg Lys Lys Val Ile Gln Glu Thr
35 40 45

Pro Val Lys Gln Ala Ala Lys Glu Ala Gly Leu Ser Ile Tyr Gln Pro
50 55 60

Glu Lys Leu Ser Gly Ser Pro Glu Met Glu Asp Leu Met Lys Leu Gly
65 70 75 80

Ala Asp Gly Ile Val Thr Ala Ala Phe Gly Gln Phe Leu Pro Ser Lys
85 90 95

Leu Leu Asp Ser Met Asp Phe Ala Val Asn Val His Ala Ser Leu Leu
100 105 110

Pro Arg His Arg Gly Gly Ala Pro Ile His Tyr Ala Leu Ile Gln Gly
115 120 125

Asp Glu Glu Ala Gly Val Thr Ile Met Glu Met Val Lys Glu Met Asp
130 135 140

Ala Gly Asp Met Ile Ser Arg Arg Ser Ile Pro Ile Thr Asp Glu Asp
145 150 155 160

Asn Val Gly Thr Leu Phe Glu Lys Leu Ala Leu Val Gly Arg Asp Leu
165 170 175

Leu Leu Asp Thr Leu Pro Ala Tyr Ile Ala Gly Asp Ile Lys Pro Glu
180 185 190

Pro Gln Asp Thr Ser Gln Val Thr Phe Ser Pro Asn Ile Lys Pro Glu
195 200 205

Glu Glu Lys Leu Asp Trp Asn Lys Thr Asn Arg Gln Leu Phe Asn Gln
210 215 220

Ile Arg Gly Met Asn Pro Trp Pro Val Ala His Thr Phe Leu Lys Gly
225 230 235 240

Asp Arg Phe Lys Ile Tyr Glu Ala Leu Pro Val Glu Gly Gln Gly Asn
245 250 255

Pro Gly Glu Ile Leu Ser Ile Gly Lys Lys Glu Leu Ile Val Ala Thr
260 265 270

Ala Glu Gly Ala Leu Ser Leu Lys Gln Val Gln Pro Ala Gly Lys Pro
275 280 285

Lys Met Asp Ile Ala Ser Phe Leu Asn Gly Val Gly Arg Thr Leu Thr
290 295 300

Val Gly Glu Arg Phe Gly Asp
305 310

<210> 216

<211> 790

<212> PRT

<213> Streptococcus pneumoniae

<400> 216

Val Phe Arg Arg Leu Gly Gln Asp Phe Gln Leu Arg Lys Val Lys Lys
1 5 10 15

Ile Leu Lys Gln Ile Asn Ala Leu Lys Gly Lys Met Ser Ser Leu Ser
20 25 30

Asp Gln Glu Leu Val Ala Lys Thr Val Glu Phe Arg Gln Arg Leu Ser
35 40 45

Glu Gly Glu Ser Leu Asp Asp Ile Leu Val Glu Ala Phe Ala Val Val
50 55 60

Arg Glu Ala Asp Lys Arg Ile Leu Gly Met Phe Pro Tyr Asp Val Gln
65 70 75 80

Val Met Gly Ala Ile Val Met His Tyr Gly Asn Val Ala Glu Met Asn
85 90 95

Thr Gly Glu Gly Lys Thr Leu Thr Ala Thr Met Pro Val Tyr Leu Asn
100 105 110

Ala Phe Ser Gly Glu Gly Val Met Val Val Thr Pro Asn Glu Tyr Leu
115 120 125

Ser Lys Arg Asp Ala Glu Glu Met Gly Gln Val Tyr Arg Phe Leu Gly
130 135 140

Leu Thr Ile Gly Val Pro Phe Thr Glu Asp Pro Lys Lys Glu Met Lys
145 150 155 160

Ala Glu Glu Lys Lys Leu Ile Tyr Ala Ser Asp Ile Ile Tyr Thr Thr
165 170 175

Asn Ser Asn Leu Gly Phe Asp Tyr Leu Asn Asp Asn Leu Ala Ser Asn
180 185 190

Glu Glu Gly Lys Phe Leu Arg Pro Phe Asn Tyr Val Ile Ile Asp Glu
195 200 205

Ile Asp Asp Ile Leu Leu Asp Ser Ala Gln Thr Pro Leu Ile Ile Ala
210 215 220

Gly Ser Pro Arg Val Gln Ser Asn Tyr Tyr Ala Ile Ile Asp Thr Leu
225 230 235 240

Val Thr Thr Leu Val Glu Gly Glu Asp Tyr Ile Phe Lys Glu Glu Lys
245 250 255

Glu Glu Val Trp Leu Thr Thr Lys Gly Ala Lys Ser Ala Glu Asn Phe
260 265 270

Leu Gly Ile Asp Asn Leu Tyr Lys Glu Glu His Ala Ser Phe Ala Arg
275 280 285

His Leu Val Tyr Ala Ile Arg Ala His Lys Leu Phe Thr Lys Asp Lys
290 295 300

Asp Tyr Ile Ile Arg Gly Asn Glu Met Val Leu Val Asp Lys Gly Thr
305 310 315 320

Gly Arg Leu Met Glu Met Thr Lys Leu Gln Gly Gly Leu His Gln Ala
325 330 335

Ile Glu Ala Lys Glu His Val Lys Leu Ser Pro Glu Thr Arg Ala Met
340 345 350

Ala Ser Ile Thr Tyr Gln Ser Leu Phe Lys Met Phe Asn Lys Ile Ser
355 360 365

Gly Met Thr Gly Thr Gly Lys Val Ala Glu Lys Glu Phe Ile Glu Thr
370 375 380

Tyr Asn Met Ser Val Val Arg Ile Pro Thr Asn Arg Pro Arg Gln Arg
385 390 395 400

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Ile Asp Tyr Pro Asp Asn Leu Tyr Ile Thr Leu Pro Glu Lys Val Tyr
                405                 410                 415

Ala Ser Leu Glu Tyr Ile Lys Gln Tyr His Ala Lys Gly Asn Pro Leu
            420                 425                 430

Leu Val Phe Val Gly Ser Val Glu Met Ser Gln Leu Tyr Ser Ser Leu
        435                 440                 445

Leu Phe Arg Glu Gly Ile Ala His Asn Val Leu Asn Ala Asn Asn Ala
    450                 455                 460

Ala Arg Glu Ala Gln Ile Ile Ser Glu Ser Gly Gln Met Gly Ala Val
465                 470                 475                 480

Thr Val Ala Thr Ser Met Ala Gly Arg Gly Thr Asp Ile Lys Leu Gly
                485                 490                 495

Lys Gly Val Ala Glu Leu Gly Gly Leu Ile Val Ile Gly Thr Glu Arg
            500                 505                 510

Met Glu Ser Gln Arg Ile Asp Leu Gln Ile Arg Gly Arg Ser Gly Arg
        515                 520                 525

Gln Gly Asp Pro Gly Met Ser Lys Phe Phe Val Ser Leu Glu Asp Asp
    530                 535                 540

Val Ile Lys Lys Phe Gly Pro Ser Trp Val His Lys Lys Tyr Lys Asp
545                 550                 555                 560

Tyr Gln Val Gln Asp Met Thr Gln Pro Glu Val Leu Lys Gly Arg Lys
                565                 570                 575

Tyr Arg Lys Leu Val Glu Lys Ala Gln His Ala Ser Asp Ser Ala Gly
            580                 585                 590

Arg Ser Ala Arg Arg Gln Thr Leu Glu Tyr Ala Glu Ser Met Asn Ile
        595                 600                 605

Gln Arg Asp Ile Val Tyr Lys Glu Arg Asn Arg Leu Ile Asp Gly Ser
    610                 615                 620

Arg Asp Leu Glu Asp Val Val Val Asp Ile Ile Glu Arg Tyr Thr Glu
625                 630                 635                 640

Glu Val Ala Ala Asp His Tyr Ala Ser Arg Glu Leu Leu Phe His Phe
                645                 650                 655

Ile Val Thr Asn Ile Ser Phe His Val Lys Glu Val Pro Asp Tyr Ile
            660                 665                 670
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Asp Val Thr Asp Lys Thr Ala Val Arg Ser Phe Met Lys Gln Val Ile
675 680 685

Asp Lys Glu Leu Ser Glu Lys Lys Glu Leu Leu Asn Gln His Asp Leu
690 695 700

Tyr Glu Gln Phe Leu Arg Leu Ser Leu Leu Lys Ala Ile Asp Asp Asn
705 710 715 720

Trp Val Glu Gln Val Asp Tyr Leu Gln Gln Leu Ser Met Ala Ile Gly
725 730 735

Gly Gln Ser Ala Ser Gln Lys Asn Pro Ile Val Glu Tyr Tyr Gln Glu
740 745 750

Ala Tyr Ala Gly Phe Glu Ala Met Lys Glu Gln Ile His Ala Asp Met
755 760 765

Val Arg Asn Leu Leu Met Gly Leu Val Glu Val Thr Pro Lys Gly Glu
770 775 780

Ile Val Thr His Phe Pro
785 790

<210> 217

<211> 4776

<212> PRT

<213> Streptococcus pneumoniae

<400> 217

Met Thr Glu Thr Val Glu Asp Lys Val Ser His Ser Ile Thr Gly Leu
1 5 10 15

Asp Ile Leu Lys Gly Ile Val Ala Ala Gly Ala Val Ile Ser Gly Thr
20 25 30

Val Ala Thr Gln Thr Lys Val Phe Thr Asn Glu Ser Ala Val Leu Glu
35 40 45

Lys Thr Val Glu Lys Thr Asp Ala Leu Ala Thr Asn Asp Thr Val Val
50 55 60

Leu Gly Thr Ile Ser Thr Ser Asn Ser Ala Ser Ser Thr Ser Leu Ser
65 70 75 80

Ala Ser Glu Ser Ala Ser Thr Ser Ala Ser Glu Ser Ala Ser Thr Ser
85 90 95

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Glu Ser Ala Ser Thr Ser
100 105 110

Ala Ser Thr Ser Ile Ser Ala Ser Ser Thr Val Val Gly Ser Gln Thr
115 120 125

Ala Ala Ala Thr Glu Ala Thr Ala Lys Lys Val Glu Glu Asp Arg Lys
130 135 140

Lys Pro Ala Ser Asp Tyr Val Ala Ser Val Thr Asn Val Asn Leu Gln
145 150 155 160

Ser Tyr Ala Lys Arg Arg Lys Arg Ser Val Asp Ser Ile Glu Gln Leu
165 170 175

Leu Ala Ser Ile Lys Asn Ala Ala Val Phe Ser Gly Asn Thr Ile Val
180 185 190

Asn Gly Ala Pro Ala Ile Asn Ala Ser Leu Asn Ile Ala Lys Ser Glu
195 200 205

Thr Lys Val Tyr Thr Gly Glu Gly Val Asp Ser Val Tyr Arg Val Pro
210 215 220

Ile Tyr Tyr Lys Leu Lys Val Thr Asn Asp Gly Ser Lys Leu Thr Phe
225 230 235 240

Thr Tyr Thr Val Thr Tyr Val Asn Pro Lys Thr Asn Asp Leu Gly Asn
245 250 255

Ile Ser Ser Met Arg Pro Gly Tyr Ser Ile Tyr Asn Ser Gly Thr Ser
260 265 270

Thr Gln Thr Met Leu Thr Leu Gly Ser Asp Leu Gly Lys Pro Ser Gly
275 280 285

Val Lys Asn Tyr Ile Thr Asp Lys Asn Gly Arg Gln Val Leu Ser Tyr
290 295 300

Asn Thr Ser Thr Met Thr Thr Gln Gly Ser Gly Tyr Thr Trp Gly Asn
305 310 315 320

Gly Ala Gln Met Asn Gly Phe Phe Ala Lys Lys Gly Tyr Gly Leu Thr
325 330 335

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Gln Ser Lys Ser Leu Ser Val Ser Ala Ser Gln Ser Ala Ser Ala Ser
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Leu Gly Ile Asp Gly Gly Phe Phe Ser Asn Leu Lys Glu Lys Ile Val
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Pro Ala Leu Tyr Ser Glu Ile Arg Glu Ile Val Ser Ser Glu Val Ala
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130 135 140

Arg Val Ser Asp Val Ala Glu Ser Thr Gly Glu Phe Thr Ser Glu Gln
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Phe Glu Lys Ala Lys Ser Gly Leu Gly Ser Gly Phe Ser Thr Val Gln
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Thr Ala Leu Ser Ser His Lys Asp Trp Glu Gln Ile Arg Gly Ala Lys
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Ile Ala Thr Ile Phe Gln Asp Pro Met Thr Ser Leu Asp Pro Ile Lys
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130 135 140

Gly Ile Pro Asp Ala Asp Arg Arg Phe Asn Glu Tyr Pro Phe Gln Tyr
145 150 155 160

Ser Gly Gly Met Arg Gln Arg Ile Val Ile Ala Ile Ala Leu Ala Cys
165 170 175

Arg Pro Asp Val Leu Ile Cys Asp Glu Pro Thr Thr Ala Leu Asp Val
180 185 190

Thr Ile Gln Ala Gln Ile Ile Asp Leu Leu Lys Ser Leu Gln Asn Glu
195 200 205

Tyr His Phe Thr Thr Ile Phe Ile Thr His Asp Leu Gly Val Val Ala
210 215 220

Ser Ile Ala Asp Lys Val Ala Val Met Tyr Ala Gly Glu Ile Val Glu
225 230 235 240

Tyr Gly Thr Val Glu Glu Val Phe Tyr Asp Pro Arg His Pro Tyr Thr
245 250 255

Trp Ser Leu Leu Ser Ser Leu Pro Gln Leu Ala Asp Asp Lys Gly Asp
260 265 270

Leu Tyr Ser Ile Pro Gly Thr Pro Pro Ser Leu Tyr Thr Asp Leu Lys
275 280 285

Gly Asp Ala Phe Ala Leu Arg Ser Asp Tyr Ala Met Gln Ile Asp Phe
290 295 300

Glu Gln Lys Ala Pro Gln Phe Ser Val Ser Glu Thr His Trp Ala Lys
305 310 315 320

Thr Trp Leu Leu His Glu Asp Ala Pro Lys Val Glu Lys Pro Ala Val
325 330 335

Ile Ala Asn Leu His Asp Lys Ile Arg Glu Lys Met Gly Phe Ala His
340 345 350

Leu Ala Asp
355

<210> 220

<211> 659

<212> PRT

<213> Streptococcus pneumoniae

<400> 220

Met Lys Lys Asn Arg Val Phe Ala Thr Ala Gly Leu Val Leu Leu Ala
1 5 10 15

Ala Gly Val Leu Ala Ala Cys Ser Ser Ser Lys Ser Ser Asp Ser Ser
20 25 30

Ala Pro Lys Ala Tyr Gly Tyr Val Tyr Thr Ala Asp Pro Glu Thr Leu
35 40 45

Asp Tyr Leu Ile Ser Ser Lys Asn Ser Thr Thr Val Val Thr Ser Asn
50 55 60

Gly Ile Asp Gly Leu Phe Thr Asn Asp Asn Tyr Gly Asn Leu Ala Pro
65 70 75 80

Ala Val Ala Glu Asp Trp Glu Val Ser Lys Asp Gly Leu Thr Tyr Thr
85 90 95

Tyr Lys Ile Arg Lys Gly Val Lys Trp Phe Thr Ser Asp Gly Glu Glu
100 105 110

Tyr Ala Glu Val Thr Ala Lys Asp Phe Val Asn Gly Leu Lys His Ala
115 120 125

Ala Asp Lys Lys Ser Glu Ala Met Tyr Leu Ala Glu Asn Ser Val Lys
130 135 140

Gly Leu Ala Asp Tyr Leu Ser Gly Thr Ser Thr Asp Phe Ser Thr Val
145 150 155 160

Gly Val Lys Ala Val Asp Asp Tyr Thr Leu Gln Tyr Thr Leu Asn Gln
165 170 175

Pro Glu Pro Phe Trp Asn Ser Lys Leu Thr Tyr Ser Ile Phe Trp Pro
180 185 190

Leu Asn Glu Glu Phe Glu Thr Ser Lys Gly Ser Asp Phe Ala Lys Pro
195 200 205

Thr Asp Pro Thr Ser Leu Leu Tyr Asn Gly Pro Phe Leu Leu Lys Gly
210 215 220

Leu Thr Ala Lys Ser Ser Val Glu Phe Val Lys Asn Glu Gln Tyr Trp
225 230 235 240

Asp Lys Glu Asn Val His Leu Asp Thr Ile Asn Leu Ala Tyr Tyr Asp
245 250 255

Gly Ser Asp Gln Glu Ser Leu Glu Arg Asn Phe Thr Ser Gly Ala Tyr
260 265 270

Ser Tyr Ala Arg Leu Tyr Pro Thr Ser Ser Asn Tyr Ser Lys Val Ala
275 280 285

Glu Glu Tyr Lys Asp Asn Ile Tyr Tyr Thr Gln Ser Gly Ser Gly Ile
290 295 300

Ala Gly Leu Gly Val Asn Ile Asp Arg Gln Ser Tyr Asn Tyr Thr Ser
305 310 315 320

Lys Thr Thr Asp Ser Glu Lys Val Ala Thr Lys Lys Ala Leu Leu Asn
325 330 335

Lys Asp Phe Arg Gln Ala Leu Asn Phe Ala Leu Asp Arg Ser Ala Tyr
340 345 350

Ser Ala Gln Ile Asn Gly Lys Asp Gly Ala Ala Leu Ala Val Arg Asn
355 360 365

Leu Phe Val Lys Pro Asp Phe Val Ser Ala Gly Glu Lys Thr Phe Gly
370 375 380

Asp Leu Val Ala Ala Gln Leu Pro Ala Tyr Gly Asp Glu Trp Lys Gly
385 390 395 400

Val Asn Leu Ala Asp Gly Gln Asp Gly Leu Phe Asn Ala Asp Lys Ala
405 410 415

Lys Ala Glu Phe Ala Lys Ala Lys Lys Ala Leu Glu Ala Asp Gly Val
420 425 430

Gln Phe Pro Ile His Leu Asp Val Pro Val Asp Gln Ala Ser Lys Asn
435 440 445

Tyr Ile Ser Arg Ile Gln Ser Phe Lys Gln Ser Val Glu Thr Val Leu
450 455 460

Gly Val Glu Asn Val Val Val Asp Ile Gln Gln Met Thr Ser Asp Glu
465 470 475 480

Phe Leu Asn Ile Thr Tyr Tyr Ala Ala Asn Ala Ser Ser Glu Asp Trp
485 490 495

Asp Val Ser Gly Gly Val Ser Trp Gly Pro Asp Tyr Gln Asp Pro Ser
500 505 510

Thr Tyr Leu Asp Ile Leu Lys Thr Thr Ser Ser Glu Thr Thr Lys Thr
515 520 525

Tyr Leu Gly Phe Asp Asn Pro Asn Ser Pro Ser Val Val Gln Val Gly
530 535 540

Leu Lys Glu Tyr Asp Lys Leu Val Asp Glu Ala Ala Arg Glu Thr Ser
545 550 555 560

Asp Leu Asn Val Arg Tyr Glu Lys Tyr Ala Ala Ala Gln Ala Trp Leu
565 570 575

Thr Asp Ser Ser Leu Phe Ile Pro Ala Met Ala Ser Ser Gly Ala Ala
580 585 590

Pro Val Leu Ser Arg Ile Val Pro Phe Thr Gly Ala Ser Ala Gln Thr
595 600 605

Gly Ser Lys Gly Ser Asp Val Tyr Phe Lys Tyr Leu Lys Ser Gln Asp
610 615 620

Lys Val Val Thr Lys Glu Glu Tyr Glu Lys Ala Arg Glu Lys Trp Leu
625 630 635 640

Lys Glu Lys Ala Glu Ser Asn Glu Lys Ala Gln Lys Glu Leu Ala Ser
645 650 655

His Val Lys

<210> 221

<211> 318

<212> PRT

<213> Streptococcus pneumoniae

<400> 221

Met Glu Ile Asn Val Ser Lys Leu Arg Thr Asp Leu Pro Gln Val Gly
1 5 10 15

Val Gln Pro Tyr Arg Gln Val His Ala His Ser Thr Gly Asn Pro His
20 25 30

Ser Thr Val Gln Asn Glu Ala Asp Tyr His Trp Arg Lys Asp Pro Glu
35 40 45

Leu Gly Phe Phe Ser His Ile Val Gly Asn Gly Cys Ile Met Gln Val
50 55 60

Gly Pro Val Asp Asn Gly Ala Trp Asp Val Gly Gly Gly Trp Asn Ala
65 70 75 80

Glu Thr Tyr Ala Ala Val Glu Leu Ile Glu Ser His Ser Thr Lys Glu
85 90 95

Glu Phe Met Thr Asp Tyr Arg Leu Tyr Ile Glu Leu Leu Arg Asn Leu
100 105 110

Ala Asp Glu Ala Gly Leu Pro Lys Thr Leu Asp Thr Gly Ser Leu Ala
115 120 125

Gly Ile Lys Thr His Glu Tyr Cys Thr Asn Asn Gln Pro Asn Asn His
130 135 140

Ser Asp His Val Asp Pro Tyr Pro Tyr Leu Ala Lys Trp Gly Ile Ser
145 150 155 160

Arg Glu Gln Phe Lys His Asp Ile Glu Asn Gly Leu Thr Ile Glu Thr
165 170 175

Gly Trp Gln Lys Asn Asp Thr Gly Tyr Trp Tyr Val His Ser Asp Gly
180 185 190

Ser Tyr Pro Lys Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr
195 200 205

Phe Asp Ser Ser Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr
210 215 220

Asp Gly Asn Trp Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly
225 230 235 240

Trp Lys Lys Ile Ala Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala
245 250 255

Met Lys Thr Gly Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp
260 265 270

Ala Lys Glu Gly Ala Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp
275 280 285

Gly Thr Gly Trp Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Lys
290 295 300

Pro Glu Phe Thr Val Glu Pro Asp Gly Leu Ile Thr Val Lys
305 310 315

<210> 222

<211> 467

<212> PRT

<213> Streptococcus pneumoniae

<400> 222

Met Lys Lys Lys Tyr Trp Thr Leu Ala Ile Leu Phe Phe Cys Leu Phe
1 5 10 15

Asn Asn Ser Val Thr Ala Gln Glu Ile Pro Lys Asn Leu Asp Gly Asn
20 25 30

Ile Thr His Thr Gln Thr Ser Glu Ser Phe Ser Glu Ser Asp Glu Lys
35 40 45

Gln Val Asp Tyr Ser Asn Lys Asn Gln Glu Glu Val Asp Gln Asn Lys
50 55 60

Phe Arg Ile Gln Ile Asp Lys Thr Glu Leu Phe Val Thr Thr Asp Lys
65 70 75 80

His Leu Glu Lys Asn Cys Cys Lys Leu Glu Leu Glu Pro Gln Ile Asn
85 90 95

Asn Asp Ile Val Asn Ser Glu Ser Asn Asn Leu Leu Gly Glu Asp Asn
100 105 110

Leu Asp Asn Lys Ile Lys Glu Asn Val Ser His Leu Asp Asn Arg Gly
115 120 125

Gly Asn Ile Glu His Asp Lys Asp Asn Leu Glu Ser Ser Ile Val Arg
130 135 140

Lys Tyr Glu Trp Asp Ile Asp Lys Val Thr Gly Gly Gly Glu Ser Tyr
145 150 155 160

Lys Leu Tyr Ser Lys Ser Asn Ser Lys Val Ser Ile Ala Ile Leu Asp
165 170 175

Ser Gly Val Asp Leu Gln Asn Thr Gly Leu Leu Lys Asn Leu Ser Asn
180 185 190

His Ser Lys Asn Tyr Val Pro Asn Lys Gly Tyr Leu Gly Lys Glu Glu
195 200 205

Gly Glu Glu Gly Ile Ile Ser Asp Ile Gln Asp Arg Leu Gly His Gly
210 215 220

Thr Ala Val Val Ala Gln Ile Val Gly Asp Asp Asn Ile Asn Gly Val
225 230 235 240

Asn Pro His Val Asn Ile Asn Val Tyr Arg Ile Phe Gly Lys Ser Ser
245 250 255

Ala Ser Pro Asp Trp Ile Val Lys Ala Ile Phe Asp Ala Val Asp Asp
260 265 270

Gly Asn Asp Ile Ile Asn Leu Ser Thr Gly Gln Tyr Leu Met Ile Asp
275 280 285

Gly Glu Tyr Glu Asp Gly Thr Asn Asp Phe Glu Thr Phe Leu Lys Tyr
290 295 300

Lys Lys Ala Ile Asp Tyr Ala Asn Gln Lys Gly Val Ile Ile Val Ala
305 310 315 320

Ala Leu Gly Asn Asp Ser Leu Asn Val Ser Asn Gln Ser Asp Leu Leu
325 330 335

Lys Leu Ile Ser Ser Arg Lys Lys Val Arg Lys Pro Gly Leu Val Val
340 345 350

Asp Val Pro Ser Tyr Phe Ser Ser Thr Ile Ser Val Gly Gly Ile Asp
355 360 365

Arg Leu Gly Asn Leu Ser Asp Phe Ser Asn Lys Gly Asp Ser Asp Ala
370 375 380

Ile Tyr Ala Pro Ala Gly Ser Thr Leu Ser Leu Ser Glu Leu Gly Leu
385 390 395 400

Asn Asn Phe Ile Asn Ala Glu Lys Tyr Lys Glu Asp Trp Ile Phe Ser
405 410 415

Ala Thr Leu Gly Gly Tyr Thr Tyr Leu Tyr Gly Asn Ser Phe Ala Ala
420 425 430

Pro Lys Val Ser Gly Ala Ile Ala Met Ile Ile Asp Lys Tyr Lys Leu
435 440 445

Lys Asp Gln Pro Tyr Asn Tyr Met Phe Val Lys Lys Phe Trp Lys Lys
450 455 460

His Tyr Gln
465

<210> 223

<211> 308

<212> PRT

<213> Streptococcus pneumoniae

<400> 223

Met Lys Lys Asp Glu Leu Phe Glu Gly Phe Tyr Leu Ile Lys Ser Ala
1 5 10 15

Asp Leu Arg Gln Thr Arg Ala Gly Lys Asn Tyr Leu Ala Phe Thr Phe
20 25 30

Gln Asp Asp Ser Gly Glu Ile Asp Gly Lys Leu Trp Asp Ala Gln Pro
35 40 45

His Asn Ile Glu Ala Phe Thr Ala Gly Lys Val Val His Met Lys Gly
50 55 60

Arg Arg Glu Val Tyr Asn Asn Thr Pro Gln Val Asn Gln Ile Thr Leu
65 70 75 80

Arg Leu Pro Gln Ala Gly Glu Pro Asn Asp Pro Ala Asp Phe Lys Val
85 90 95

Lys Ser Pro Val Asp Val Lys Glu Ile Arg Asp Tyr Met Ser Gln Met
100 105 110

Ile Phe Lys Ile Glu Asn Pro Val Trp Gln Arg Ile Val Arg Asn Leu
115 120 125

Tyr Thr Lys Tyr Asp Lys Glu Phe Tyr Ser Tyr Pro Ala Ala Lys Thr
130 135 140

Asn His His Ala Phe Glu Thr Gly Leu Ala Tyr His Thr Ala Thr Met
145 150 155 160

Val Arg Leu Ala Asp Ala Ile Ser Glu Val Tyr Pro Gln Leu Asn Lys
165 170 175

Ser Leu Leu Tyr Ala Gly Ile Met Leu His Asp Leu Ala Lys Val Ile
180 185 190

Glu Leu Thr Gly Pro Asp Gln Thr Glu Tyr Thr Val Arg Gly Asn Leu
195 200 205

Leu Gly His Ile Ala Leu Ile Asp Ser Glu Ile Thr Lys Thr Val Met
210 215 220

Glu Leu Gly Ile Asp Asp Thr Lys Glu Glu Val Val Leu Leu Arg His
225 230 235 240

Val Ile Leu Ser His His Gly Leu Leu Glu Tyr Gly Ser Pro Val Arg
245 250 255

Pro Arg Ile Met Glu Ala Glu Ile Ile His Met Ile Asp Asn Leu Asp
260 265 270

Ala Ser Met Met Met Met Ser Thr Ala Leu Ala Leu Val Asp Lys Gly
275 280 285

Glu Met Thr Asn Lys Ile Phe Ala Met Asp Asn Arg Ser Phe Tyr Lys
290 295 300

Pro Asp Leu Asp
305

<210> 224

<211> 221

<212> PRT

<213> Streptococcus pneumoniae

<400> 224

Val Thr Ile Leu Gly Lys Asp Thr Val Gln Gln Ser Ala Lys Gly Glu
1 5 10 15

Ser Val Thr Gln Glu Ala Thr Pro Glu Tyr Lys Leu Glu Asn Thr Pro
20 25 30

Gly Gly Asp Lys Gly Gly Asn Thr Gly Ser Ser Asp Ala Asn Ala Asn
35 40 45

Glu Gly Gly Gly Ser Gln Ala Gly Gly Ser Ala His Thr Gly Ser Gln
50 55 60

Asn Ser Ala Gln Ser Gln Ala Ser Lys Gln Leu Ala Thr Glu Lys Glu
65 70 75 80

Ser Ala Lys Asn Ala Ile Glu Lys Ala Ala Lys Asp Lys Gln Asp Glu
85 90 95

Ile Lys Gly Ala Pro Leu Ser Asp Lys Glu Lys Ala Glu Leu Leu Ala
100 105 110

Arg Val Glu Ala Glu Lys Gln Ala Ala Leu Lys Glu Ile Glu Asn Ala
115 120 125

Lys Thr Met Glu Asp Val Lys Glu Ala Glu Thr Ile Gly Val Gln Ala
130 135 140

Ile Ala Met Val Thr Val Pro Lys Arg Pro Val Ala Pro Asn Ala Ala
145 150 155 160

Pro Lys Thr Thr Ser Ala Pro Gln Ala Thr Ala Gly Thr Met Gln Asp
165 170 175

Val Thr Tyr Gln Ser Pro Ala Gly Lys Gln Leu Pro Asn Thr Gly Ser
180 185 190

Ala Ser Ser Ala Ala Leu Ala Ser Leu Gly Leu Val Val Ala Thr Ser
195 200 205

Gly Phe Ala Leu Leu Gly Arg Lys Thr Arg Arg Arg Lys
210 215 220

<210> 225

<211> 336

<212> PRT

<213> Streptococcus pneumoniae

<400> 225

Met Asn Ala Asp Asp Thr Val Thr Ile Tyr Asp Val Ala Arg Glu Ala
1   5   10   15

Gly Val Ser Met Ala Thr Val Ser Arg Val Val Asn Gly Asn Lys Asn
            20   25   30

Val Lys Glu Asn Thr Arg Lys Lys Val Leu Glu Val Ile Asp Arg Leu
        35   40   45

Asp Tyr Arg Pro Asn Ala Val Ala Arg Gly Leu Ala Ser Lys Lys Thr
    50   55   60

Thr Thr Val Gly Val Val Ile Pro Asn Ile Thr Asn Gly Tyr Phe Ser
65   70   75   80

Ser Leu Ala Lys Gly Ile Asp Asp Ile Ala Glu Met Tyr Lys Tyr Asn
                85   90   95

Ile Val Leu Ala Asn Ser Asp Glu Asp Asn Glu Lys Glu Val Ser Val
            100   105   110

Val Asn Thr Leu Phe Ser Lys Gln Val Asp Gly Ile Ile Tyr Met Gly
        115   120   125

Tyr His Leu Thr Asp Lys Ile Arg Ser Glu Phe Ser Arg Ser Arg Thr
    130   135   140

Pro Ile Val Leu Ala Gly Thr Val Asp Val Glu His Gln Leu Pro Ser
145   150   155   160

Val Asn Ile Asp Tyr Lys Gln Ala Thr Ile Asp Ala Val Ser Tyr Leu
                165   170   175

Ala Lys Glu Asn Glu Arg Ile Ala Phe Val Ser Gly Pro Leu Val Asp
            180   185   190

Asp Ile Asn Gly Lys Val Arg Leu Val Gly Tyr Lys Glu Thr Leu Lys
        195   200   205

Lys Ala Gly Ile Thr Tyr Ser Glu Gly Leu Val Phe Glu Ser Lys Tyr
    210   215   220

Ser Tyr Asp Asp Gly Tyr Ala Leu Ala Glu Arg Leu Ile Ser Ser Asn
225   230   235   240

Ala Thr Ala Ala Val Val Thr Gly Asp Glu Leu Ala Ala Gly Val Leu
245 250 255

Asn Gly Leu Ala Asp Lys Gly Val Ser Val Pro Glu Asp Phe Glu Ile
260 265 270

Ile Thr Ser Asp Asp Ser Gln Ile Ser Arg Phe Thr Arg Pro Asn Leu
275 280 285

Thr Thr Ile Ala Gln Pro Leu Tyr Asp Leu Gly Ala Ile Ser Met Arg
290 295 300

Met Leu Thr Lys Ile Met His Lys Glu Glu Leu Glu Glu Arg Glu Val
305 310 315 320

Leu Leu Pro His Gly Leu Thr Glu Arg Ser Ser Thr Arg Lys Arg Lys
325 330 335

<210> 226

<211> 469

<212> PRT

<213> Streptococcus pneumoniae

<400> 226

Met Lys Lys Lys Leu Val Phe Pro Asn Leu Phe Trp Trp Gly Ala Ala
1 5 10 15

Ser Ser Gly Pro Gln Thr Glu Gly Gln Tyr Gly Lys Val His Glu Asn
20 25 30

Val Met Asp Tyr Trp Phe Lys Thr His Pro Glu Asp Phe Phe Asp Asn
35 40 45

Val Gly Pro Leu Val Ala Ser Asn Phe Phe His Thr Tyr Thr Glu Asp
50 55 60

Phe His Leu Met Lys Glu Ile Gly Val Asn Ser Phe Arg Thr Ser Ile
65 70 75 80

Gln Trp Ser Arg Leu Ile Lys Asn Leu Glu Thr Gly Glu Pro Asp Pro
85 90 95

Lys Gly Ile Ala Phe Tyr Asn Ala Ile Ile Glu Glu Ala Lys Lys Asn
100 105 110

Gln Met Asp Leu Val Met Asn Leu His His Phe Asp Leu Pro Val Glu
115 120 125

Leu Leu Gln Lys Tyr Gly Gly Trp Glu Ser Lys His Val Val Glu Leu
130 135 140

Phe Val Lys Phe Ala Lys Thr Ala Phe Thr Cys Phe Gly Asp Lys Val
145 150 155 160

His Tyr Trp Thr Thr Phe Asn Glu Pro Met Val Ile Pro Glu Ala Gly
165 170 175

Tyr Leu Tyr Ala Phe His Tyr Pro Asn Leu Lys Gly Lys Gly Lys Glu
180 185 190

Ala Val Gln Val Ile Tyr Asn Leu Asn Leu Ala Ser Ala Lys Val Ile
195 200 205

Gln Leu Tyr Arg Ser Leu Glu Leu Asp Gly Lys Ile Gly Ile Ile Leu
210 215 220

Asn Leu Thr Pro Ala Tyr Pro Arg Ser Asn Ser Pro Glu Asp Leu Glu
225 230 235 240

Ala Ser Arg Phe Thr Asp Asp Phe Phe Asn Lys Val Phe Leu Asn Pro
245 250 255

Ala Val Lys Gly Thr Phe Pro Glu Arg Leu Val Lys Gln Leu Glu Arg
260 265 270

Asp Gly Val Leu Trp Ser His Thr Glu Lys Glu Leu Gln Leu Met Lys
275 280 285

Ser Asn Thr Val Asp Phe Leu Gly Val Asn Tyr Tyr His Pro Lys Arg
290 295 300

Val Gln Ala Gln Ala Asn Pro Glu Glu Tyr Gln Thr Pro Trp Met Pro
305 310 315 320

Asp Gln Tyr Phe Lys Glu Tyr Glu Trp Leu Glu Arg Arg Met Asn Pro
325 330 335

Tyr Arg Gly Trp Glu Ile Phe Pro Lys Ala Ile Tyr Asp Ile Ala Met
340 345 350

Ile Val Lys Glu Glu Tyr Gly Asn Ile Pro Trp Phe Ile Ser Glu Asn
355 360 365

Gly Met Gly Val Glu Asn Glu Ala Arg Phe Ile Asp Glu Asn Gly Val
370 375 380

Ile Asp Asp Val Tyr Arg Ile Glu Phe Tyr Glu Glu His Leu Arg Trp
385 390 395 400

Leu His Lys Ala Ile Glu Glu Gly Ser His Cys Phe Gly Tyr His Ala
405 410 415

Trp Thr Ala Phe Asp Cys Trp Ser Trp Asn Asn Ala Tyr Lys Asn Arg
420 425 430

Tyr Gly Phe Ile Ser Val Asp Leu Glu Thr Gln Lys Arg Thr Ile Lys
435 440 445

Ser Ser Gly Arg Trp Tyr Arg Lys Val Ser Asp Asn Asn Gly Phe Glu
450 455 460

Val Glu Ile Glu Glu
465

<210> 227

<211> 136

<212> PRT

<213> Streptococcus pneumoniae

<400> 227

Val Glu Asn Leu Thr Asn Phe Tyr Glu Lys Tyr Arg Val Tyr Leu Thr
1 5 10 15

Arg Pro Arg Leu Glu Leu Leu Ala Val Val Thr Ile Val Phe Cys Ala
20 25 30

Val Leu Val Phe Phe Leu Asn Ile Pro Gly Lys Gly Val Leu Lys Leu
35 40 45

Asp Asn Gly Thr Ile Val Tyr Asp Gly Ser Leu Val Arg Gly Lys Met
50 55 60

Asn Gly Gln Gly Thr Ile Thr Phe Gln Asn Gly Asp Gln Tyr Thr Gly
65 70 75 80

Gly Phe Asn Asn Gly Ala Phe Asn Gly Lys Gly Thr Phe Gln Ser Lys
85 90 95

Glu Gly Trp Thr Tyr Glu Gly Asp Phe Val Asn Gly Gln Ala Glu Gly
100 105 110

Lys Gly Lys Leu Thr Thr Glu Gln Glu Val Val Tyr Glu Gly Thr Phe
115 120 125

Lys Gln Gly Val Phe Gln Gln Lys
130 135

<210> 228

<211> 207

<212> PRT

<213> Streptococcus pneumoniae

<400> 228

Met Leu Asn Lys Ile Arg Asp Tyr Leu Asp Phe Ala Gly Leu Gln Tyr
1   5   10   15

Arg Asn Pro Asp Lys Ala Gly Ala Glu Arg Glu Lys Met Leu Ala Phe
            20   25   30

Arg His Lys Gly Gln Glu Ala Arg Lys Val Phe Thr Glu Leu Ala Lys
        35   40   45

Ala Phe Gln Ala Ser His Pro Glu Trp Gln Leu Gln Gln Thr Ser Gln
    50   55   60

Trp Met Asn Gln Ala Gln Arg Leu Arg Pro His Phe Trp Val Tyr Leu
65   70   75   80

Gln Arg Asp Gly Gln Val Thr Glu Pro Met Met Ala Leu Arg Leu Tyr
                85   90   95

Gly Thr Ser Thr Asp Phe Gly Ile Ser Leu Glu Val Ser Phe Ile Glu
            100   105   110

Arg Lys Lys Asp Glu Gln Thr Leu Gly Lys Gln Ala Lys Val Leu Asp
        115   120   125

Ile Pro Thr Val Lys Gly Ile Tyr Tyr Leu Thr Tyr Ser Asn Gly Gln
    130   135   140

Ser Gln Arg Trp Glu Ala Asn Glu Glu Lys Arg Arg Thr Leu Arg Glu
145   150   155   160

Lys Val Arg Ser Gln Glu Val Arg Lys Val Leu Val Lys Val Asp Val
                165   170   175

Pro Met Thr Glu Asn Ser Ser Glu Glu Glu Ile Val Glu Gly Leu Leu
            180   185   190

Lys Ser Tyr Ser Lys Ile Leu Pro Tyr Tyr Leu Ala Thr Arg Lys
        195   200   205

<210> 229

<211> 153

<212> PRT

<213> Streptococcus pneumoniae

<400> 229

Met Val Gln Asn Ser Cys Trp Gln Ser Lys Ser His Lys Val Lys Ala
1 5 10 15

Phe Thr Leu Leu Glu Ser Leu Leu Ala Leu Ile Val Ile Ser Gly Gly
20 25 30

Leu Leu Leu Phe Gln Ala Met Ser Gln Leu Leu Ile Ser Glu Val Arg
35 40 45

Tyr Gln Gln Gln Ser Glu Gln Lys Glu Trp Leu Leu Phe Val Asp Gln
50 55 60

Leu Glu Val Glu Leu Asp Arg Ser Gln Phe Glu Lys Val Glu Gly Asn
65 70 75 80

Arg Leu Tyr Met Lys Gln Asp Gly Lys Asp Ile Ala Ile Gly Lys Ser
85 90 95

Lys Ser Asp Asp Phe Arg Lys Thr Asn Ala Arg Gly Arg Gly Tyr Gln
100 105 110

Pro Met Val Tyr Gly Leu Lys Ser Val Arg Ile Thr Glu Asp Asn Gln
115 120 125

Leu Val Arg Phe His Phe Gln Phe Gln Lys Gly Leu Glu Arg Glu Phe
130 135 140

Ile Tyr Arg Val Glu Lys Glu Lys Ser
145 150

<210> 230

<211> 108

<212> PRT

<213> Streptococcus pneumoniae

<400> 230

Met Lys Lys Met Met Thr Phe Leu Lys Lys Ala Lys Val Lys Ala Phe
1 5 10 15

Thr Leu Val Glu Met Leu Val Val Leu Leu Ile Ile Ser Val Leu Phe
20 25 30

Leu Leu Phe Val Pro Asn Leu Thr Lys Gln Lys Glu Ala Val Asn Asp
35 40 45

Lys Gly Lys Ala Ala Val Val Lys Val Val Glu Ser Gln Ala Glu Leu
50 55 60

Tyr Ser Leu Glu Lys Asn Glu Asp Ala Ser Leu Arg Lys Leu Gln Ala
65 70 75 80

Asp Gly Arg Ile Thr Glu Glu Gln Ala Lys Ala Tyr Lys Glu Tyr Asn
85 90 95

Asp Lys Asn Gly Gly Ala Asn Arg Lys Val Asn Asp
100 105

<210> 231

<211> 299

<212> PRT

<213> Streptococcus pneumoniae

<400> 231

Met Thr Ser Lys Val Arg Lys Ala Val Ile Pro Ala Ala Gly Leu Gly
1 5 10 15

Thr Arg Phe Leu Pro Ala Thr Lys Ala Leu Ala Lys Glu Met Leu Pro
20 25 30

Ile Val Asp Lys Pro Thr Ile Gln Phe Ile Val Glu Glu Ala Leu Lys
35 40 45

Ser Gly Ile Glu Asp Ile Leu Val Val Thr Gly Lys Ser Lys Arg Ser
50 55 60

Ile Glu Asp His Phe Asp Ser Asn Phe Glu Leu Glu Tyr Asn Leu Lys
65 70 75 80

Glu Lys Gly Lys Thr Asp Leu Leu Lys Leu Val Asp Lys Thr Thr Asp
85 90 95

Met Arg Leu His Phe Ile Arg Gln Thr His Pro Arg Gly Leu Gly Asp
100 105 110

Ala Val Leu Gln Ala Lys Ala Phe Val Gly Asn Glu Pro Phe Val Val
115 120 125

Met Leu Gly Asp Asp Leu Met Asp Ile Thr Asp Glu Lys Ala Val Pro
130 135 140

Leu Thr Lys Gln Leu Met Asp Asp Tyr Glu Arg Thr His Ala Ser Thr
145 150 155 160

Ile Ala Val Met Pro Val Pro His Asp Glu Val Ser Ala Tyr Gly Val
165 170 175

Ile Ala Pro Gln Gly Glu Gly Lys Asp Gly Leu Tyr Ser Val Glu Thr
180 185 190

Phe Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Asp Leu Ala Ile
195 200 205

Ile Gly Arg Tyr Leu Leu Thr Pro Glu Ile Phe Glu Ile Leu Glu Lys
210 215 220

Gln Ala Pro Gly Ala Gly Asn Glu Ile Gln Leu Thr Asp Ala Ile Asp
225 230 235 240

Thr Leu Asn Lys Thr Gln Arg Val Phe Ala Arg Glu Phe Lys Gly Ala
245 250 255

Arg Tyr Asp Val Gly Asp Lys Phe Gly Phe Met Lys Thr Ser Ile Asp
260 265 270

Tyr Ala Leu Lys His Pro Gln Val Lys Asp Asp Leu Lys Asn Tyr Leu
275 280 285

Ile Gln Leu Gly Lys Glu Leu Thr Glu Lys Glu
290 295

<210> 232

<211> 821

<212> PRT

<213> Streptococcus pneumoniae

<400> 232

Met Gln Asn Gln Leu Asn Glu Leu Lys Arg Lys Met Leu Glu Phe Phe
1 5 10 15

Gln Gln Lys Gln Lys Asn Lys Lys Ser Ala Arg Pro Gly Lys Lys Gly
20 25 30

Ser Ser Thr Lys Lys Ser Lys Thr Leu Asp Lys Ser Val Ile Phe Pro
35 40 45

Ala Ile Leu Leu Ser Ile Lys Ala Leu Phe Asn Leu Leu Phe Val Leu
50 55 60

Gly Phe Leu Gly Gly Met Leu Gly Ala Gly Ile Ala Leu Gly Tyr Gly
65 70 75 80

Val Ala Leu Phe Asp Lys Val Arg Val Pro Gln Thr Glu Glu Leu Val
85 90 95

Asn Gln Val Lys Asp Ile Ser Ser Ile Ser Glu Ile Thr Tyr Ser Asp
100 105 110

Gly Thr Val Ile Ala Ser Ile Glu Ser Asp Leu Leu Arg Thr Ser Ile
115 120 125

Ser Ser Glu Gln Ile Ser Glu Asn Leu Lys Lys Ala Ile Ile Ala Thr
130 135 140

Glu Asp Glu His Phe Lys Glu His Lys Gly Val Val Pro Lys Ala Val
145 150 155 160

Ile Arg Ala Thr Leu Gly Lys Phe Val Gly Leu Gly Ser Ser Ser Gly
165 170 175

Gly Ser Thr Leu Thr Gln Gln Leu Ile Lys Gln Gln Val Val Gly Asp
180 185 190

Ala Pro Thr Leu Ala Arg Lys Ala Ala Glu Ile Val Asp Ala Leu Ala
195 200 205

Leu Glu Arg Ala Met Asn Lys Asp Glu Ile Leu Thr Thr Tyr Leu Asn
210 215 220

Val Ala Pro Phe Gly Arg Asn Asn Lys Gly Gln Asn Ile Ala Gly Ala
225 230 235 240

Arg Gln Ala Ala Glu Gly Ile Phe Gly Val Asp Ala Ser Gln Leu Thr
245 250 255

Val Pro Gln Ala Ala Phe Leu Ala Gly Leu Pro Gln Ser Pro Ile Thr
260 265 270

Tyr Ser Pro Tyr Glu Asn Thr Gly Glu Leu Lys Ser Asp Glu Asp Leu
275 280 285

Glu Ile Gly Leu Arg Arg Ala Lys Ala Val Leu Tyr Ser Met Tyr Arg
290 295 300

Thr Gly Ala Leu Ser Lys Asp Glu Tyr Ser Gln Tyr Lys Asp Tyr Asp
305 310 315 320

Leu Lys Gln Asp Phe Leu Pro Ser Gly Thr Val Thr Gly Ile Ser Arg
325 330 335

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Asp Tyr Leu Tyr Phe Thr Thr Leu Ala Glu Ala Gln Glu Arg Met Tyr
            340                 345                 350

Asp Tyr Leu Ala Gln Arg Asp Asn Val Ser Ala Lys Glu Leu Lys Asn
        355                 360                 365

Glu Ala Thr Gln Lys Phe Tyr Arg Asp Leu Ala Ala Lys Glu Ile Glu
    370                 375                 380

Asn Gly Gly Tyr Lys Ile Thr Thr Thr Ile Asp Gln Lys Ile His Ser
385                 390                 395                 400

Ala Met Gln Ser Ala Val Ala Asp Tyr Gly Tyr Leu Leu Asp Asp Gly
                405                 410                 415

Thr Gly Arg Val Glu Val Gly Asn Val Leu Met Asp Asn Gln Thr Gly
            420                 425                 430

Ala Ile Leu Gly Phe Val Gly Gly Arg Asn Tyr Gln Glu Asn Gln Asn
        435                 440                 445

Asn His Ala Phe Asp Thr Lys Arg Ser Pro Ala Ser Thr Thr Lys Pro
    450                 455                 460

Leu Leu Ala Tyr Gly Ile Ala Ile Asp Gln Gly Leu Met Gly Ser Glu
465                 470                 475                 480

Thr Ile Leu Ser Asn Tyr Pro Thr Asn Phe Ala Asn Gly Asn Pro Ile
                485                 490                 495

Met Tyr Ala Asn Ser Lys Gly Thr Gly Met Met Thr Leu Gly Glu Ala
            500                 505                 510

Leu Asn Tyr Ser Trp Asn Ile Pro Ala Tyr Trp Thr Tyr Arg Met Leu
        515                 520                 525

Arg Glu Lys Gly Val Asp Val Lys Gly Tyr Met Glu Lys Met Gly Tyr
    530                 535                 540

Glu Ile Pro Glu Tyr Gly Ile Glu Ser Leu Pro Met Gly Gly Gly Ile
545                 550                 555                 560

Glu Val Thr Val Ala Gln His Thr Asn Gly Tyr Gln Thr Leu Ala Asn
                565                 570                 575

Asn Gly Val Tyr His Gln Lys His Val Ile Ser Lys Ile Glu Ala Ala
            580                 585                 590

Asp Gly Arg Val Val Tyr Glu Tyr Gln Asp Lys Pro Val Gln Val Tyr
        595                 600                 605
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Ser Lys Ala Thr Ala Thr Ile Met Gln Gly Leu Leu Arg Glu Val Leu
610 615 620

Ser Ser Arg Val Thr Thr Thr Phe Lys Ser Asn Leu Thr Ser Leu Asn
625 630 635 640

Pro Thr Leu Ala Asn Ala Asp Trp Ile Gly Lys Thr Gly Thr Thr Asn
645 650 655

Gln Asp Glu Asn Met Trp Leu Met Leu Ser Thr Pro Arg Leu Thr Leu
660 665 670

Gly Gly Trp Ile Gly His Asp Asp Asn His Ser Leu Ser Arg Arg Ala
675 680 685

Gly Tyr Ser Asn Asn Ser Asn Tyr Met Ala His Leu Val Asn Ala Ile
690 695 700

Gln Gln Ala Ser Pro Ser Ile Trp Gly Asn Glu Arg Phe Ala Leu Asp
705 710 715 720

Pro Ser Val Val Lys Ser Glu Val Leu Lys Ser Thr Gly Gln Lys Pro
725 730 735

Glu Lys Val Ser Val Glu Gly Lys Glu Val Glu Val Thr Gly Ser Thr
740 745 750

Val Thr Ser Tyr Trp Ala Asn Lys Ser Gly Ala Pro Ala Thr Ser Tyr
755 760 765

Arg Phe Ala Ile Gly Gly Ser Asp Ala Asp Tyr Gln Asn Ala Trp Ser
770 775 780

Ser Ile Val Gly Ser Leu Pro Thr Pro Ser Ser Ser Ser Ser Ser Ser
785 790 795 800

Ser Ser Ser Ser Asp Ser Ser Asn Ser Ser Thr Thr Arg Pro Ser Ser
805 810 815

Ser Arg Ala Arg Arg
820

<210> 233

<211> 423

<212> PRT

<213> Streptococcus pneumoniae

<400> 233

Met Ser Ser Lys Phe Met Lys Ser Ala Ala Val Leu Gly Thr Ala Thr
1   5   10   15

Leu Ala Ser Leu Leu Leu Val Ala Cys Gly Ser Lys Thr Ala Asp Lys
            20   25   30

Pro Ala Asp Ser Gly Ser Ser Glu Val Lys Glu Leu Thr Val Tyr Val
        35   40   45

Asp Glu Gly Tyr Lys Ser Tyr Ile Glu Glu Val Ala Lys Ala Tyr Glu
    50   55   60

Lys Glu Ala Gly Val Lys Val Thr Leu Lys Thr Gly Asp Ala Leu Gly
65   70   75   80

Gly Leu Asp Lys Leu Ser Leu Asp Asn Gln Ser Gly Asn Val Pro Asp
                85   90   95

Val Met Met Ala Pro Tyr Asp Arg Val Gly Ser Leu Gly Ser Asp Gly
            100   105   110

Gln Leu Ser Glu Val Lys Leu Ser Asp Gly Ala Lys Thr Asp Asp Thr
        115   120   125

Thr Lys Ser Leu Val Thr Ala Ala Asn Gly Lys Val Tyr Gly Ala Pro
    130   135   140

Ala Val Ile Glu Ser Leu Val Met Tyr Tyr Asn Lys Asp Leu Val Lys
145   150   155   160

Asp Ala Pro Lys Thr Phe Ala Asp Leu Glu Asn Leu Ala Lys Asp Ser
                165   170   175

Lys Tyr Ala Phe Ala Gly Glu Asp Gly Lys Thr Thr Ala Phe Leu Ala
            180   185   190

Asp Trp Thr Asn Phe Tyr Tyr Thr Tyr Gly Leu Leu Ala Gly Asn Gly
        195   200   205

Ala Tyr Val Phe Gly Gln Asn Gly Lys Asp Ala Lys Asp Ile Gly Leu
    210   215   220

Ala Asn Asp Gly Ser Ile Val Gly Ile Asn Tyr Ala Lys Ser Trp Tyr
225   230   235   240

Glu Lys Trp Pro Lys Gly Met Gln Asp Thr Glu Gly Ala Gly Asn Leu
                245   250   255

Ile Gln Thr Gln Phe Gln Glu Gly Lys Thr Ala Ala Ile Ile Asp Gly
            260   265   270

Pro Trp Lys Ala Gln Ala Phe Lys Asp Ala Lys Val Asn Tyr Gly Val
275 280 285

Ala Thr Ile Pro Thr Leu Pro Asn Gly Lys Glu Tyr Ala Ala Phe Gly
290 295 300

Gly Gly Lys Ala Trp Val Ile Pro Gln Ala Val Lys Asn Leu Glu Ala
305 310 315 320

Ser Gln Lys Phe Val Asp Phe Leu Val Ala Thr Glu Gln Gln Lys Val
325 330 335

Leu Tyr Asp Lys Thr Asn Glu Ile Pro Ala Asn Thr Glu Ala Arg Ser
340 345 350

Tyr Ala Glu Gly Lys Asn Asp Glu Leu Thr Thr Ala Val Ile Lys Gln
355 360 365

Phe Lys Asn Thr Gln Pro Leu Pro Asn Ile Ser Gln Met Ser Ala Val
370 375 380

Trp Asp Pro Ala Lys Asn Met Leu Phe Asp Ala Val Ser Gly Gln Lys
385 390 395 400

Asp Ala Lys Thr Ala Ala Asn Asp Ala Val Thr Leu Ile Lys Glu Thr
405 410 415

Ile Lys Gln Lys Phe Gly Glu
420

<210> 234

<211> 155

<212> PRT

<213> Streptococcus pneumoniae

<400> 234

Met Ile Asp Lys Val Val Arg Asn Leu Leu Leu Thr Phe Phe Phe Cys
1 5 10 15

Lys Met Thr Lys Ile Ile Ile Phe Leu Thr Thr Ile Leu Val Lys Lys
20 25 30

Lys Lys Ile Cys Tyr Asn Glu Phe Lys Leu Arg Asn Arg Lys Gln Lys
35 40 45

Gly Val Ile Met Trp Val Leu Gly Phe Ile Leu Phe Met Ile Phe Phe
50 55 60

Tyr Ser Asn Asn Ser Lys Lys Ile Lys Lys Leu Glu Asn Lys Ile Lys
65 70 75 80

Arg Leu Glu Arg Lys Glu Lys Gly Asn Ala Glu Met Ser Arg Leu Leu
85 90 95

Gln Glu Met Ile Gly Lys Glu Pro Ile Ile Thr Gly Val Tyr Ile Gly
100 105 110

Pro Asp Asn Trp Glu Val Val Asp Val Asp Glu Glu Trp Val Lys Leu
115 120 125

Arg Arg Val Asp Asn Thr Gly Lys Glu Lys Phe Lys Leu Gln Arg Ile
130 135 140

Glu Asp Ile Gln Thr Val Glu Phe Asp Gly Glu
145 150 155

<210> 235

<211> 285

<212> PRT

<213> Streptococcus pneumoniae

<400> 235

Met Ile Leu Ser Lys Asn Arg Glu Asp Gly Leu Arg Lys Phe Ala Thr
1 5 10 15

Asn Ile Arg Leu Asn Thr Leu Arg Thr Leu Asn His Leu Gly Phe Gly
20 25 30

His Tyr Gly Gly Ser Leu Ser Ile Val Glu Val Leu Ala Val Leu Tyr
35 40 45

Gly Glu Ile Met Pro Met Thr Pro Glu Ile Phe Ala Ala Arg Asp Arg
50 55 60

Asp Tyr Phe Ile Leu Ser Lys Gly His Gly Gly Pro Ala Leu Tyr Ser
65 70 75 80

Thr Leu Tyr Leu Asn Gly Phe Phe Asp Lys Glu Phe Leu Tyr Ser Leu
85 90 95

Asn Thr Asn Gly Thr Lys Leu Pro Ser His Pro Asp Arg Asn Leu Thr
100 105 110

Pro Gly Ile Asp Met Thr Thr Gly Ser Leu Gly Gln Gly Ile Ser Val
115 120 125

Ala Thr Gly Leu Ala Tyr Gly Gln Arg Ile Arg Lys Ser Pro Phe Tyr
130 135 140

Thr Tyr Ala Ile Val Gly Asp Gly Glu Leu Asn Glu Gly Gln Cys Trp
145 150 155 160

Glu Ala Ile Gln Phe Ala Ser His Gln Gln Leu Ser Asn Leu Ile Val
165 170 175

Phe Val Asp Asp Asn Lys Lys Gln Leu Asp Gly Phe Thr Lys Asp Ile
180 185 190

Cys Asn Pro Gly Asp Phe Val Glu Lys Phe Ser Ala Phe Gly Phe Glu
195 200 205

Ser Ile Arg Val Lys Gly Ser Asp Ile Arg Glu Ile Tyr Glu Gly Ile
210 215 220

Val Gln Leu Lys Gln Ser Asn Asn Ser Ser Pro Lys Cys Ile Val Leu
225 230 235 240

Asp Thr Ile Lys Gly Gln Gly Val Gln Glu Leu Glu Glu Met Lys Ser
245 250 255

Asn His His Leu Arg Pro Thr Val Glu Glu Lys Gln Met Leu Thr Ser
260 265 270

Val Val Glu Arg Leu Ser Gln Glu Leu Glu Glu Thr Glu
275 280 285

<210> 236

<211> 621

<212> PRT

<213> Streptococcus pneumoniae

<400> 236

Met Lys Lys Thr Thr Ile Leu Ser Leu Thr Thr Ala Ala Val Ile Leu
1 5 10 15

Ala Ala Tyr Val Pro Asn Glu Pro Ile Leu Ala Asp Thr Pro Ser Ser
20 25 30

Glu Val Ile Lys Glu Thr Lys Val Gly Ser Ile Ile Gln Gln Asn Asn
35 40 45

Ile Lys Tyr Lys Val Leu Thr Val Glu Gly Asn Ile Gly Thr Val Gln
50 55 60

Val Gly Asn Gly Val Thr Pro Val Glu Phe Glu Ala Gly Gln Asp Gly
65 70 75 80

Lys Pro Phe Thr Ile Pro Thr Lys Ile Thr Val Gly Asp Lys Val Phe
85 90 95

Thr Val Thr Glu Val Ala Ser Gln Ala Phe Ser Tyr Tyr Pro Asp Glu
100 105 110

Thr Gly Arg Ile Val Tyr Tyr Pro Ser Ser Ile Thr Ile Pro Ser Ser
115 120 125

Ile Lys Lys Ile Gln Lys Lys Gly Phe His Gly Ser Lys Ala Lys Thr
130 135 140

Ile Ile Phe Asp Lys Gly Ser Gln Leu Glu Lys Ile Glu Asp Arg Ala
145 150 155 160

Phe Asp Phe Ser Glu Leu Glu Glu Ile Glu Leu Pro Ala Ser Leu Glu
165 170 175

Tyr Ile Gly Thr Ser Ala Phe Ser Phe Ser Gln Lys Leu Lys Lys Leu
180 185 190

Thr Phe Ser Ser Ser Ser Lys Leu Glu Leu Ile Ser His Glu Ala Phe
195 200 205

Ala Asn Leu Ser Asn Leu Glu Lys Leu Thr Leu Pro Lys Ser Val Lys
210 215 220

Thr Leu Gly Ser Asn Leu Phe Arg Leu Thr Thr Ser Leu Lys His Val
225 230 235 240

Asp Val Glu Glu Gly Asn Glu Ser Phe Ala Ser Val Asp Gly Val Leu
245 250 255

Phe Ser Lys Asp Lys Thr Gln Leu Ile Tyr Tyr Pro Ser Gln Lys Asn
260 265 270

Asp Glu Ser Tyr Lys Thr Pro Lys Glu Thr Lys Glu Leu Ala Ser Tyr
275 280 285

Ser Phe Asn Lys Asn Ser Tyr Leu Lys Lys Leu Glu Leu Asn Glu Gly
290 295 300

Leu Glu Lys Ile Gly Thr Phe Ala Phe Ala Asp Ala Ile Lys Leu Glu
305 310 315 320

Glu Ile Ser Leu Pro Asn Ser Leu Glu Thr Ile Glu Arg Leu Ala Phe
325 330 335

Tyr Gly Asn Leu Glu Leu Lys Glu Leu Ile Leu Pro Asp Asn Val Lys
340 345 350

Asn Phe Gly Lys His Val Met Asn Gly Leu Pro Lys Leu Lys Ser Leu
355 360 365

Thr Ile Gly Asn Asn Ile Asn Ser Leu Pro Ser Phe Phe Leu Ser Gly
370 375 380

Val Leu Asp Ser Leu Lys Glu Ile His Ile Lys Asn Lys Ser Thr Glu
385 390 395 400

Phe Ser Val Lys Lys Asp Thr Phe Ala Ile Pro Glu Thr Val Lys Phe
405 410 415

Tyr Val Thr Ser Glu His Ile Lys Asp Val Leu Lys Ser Asn Leu Ser
420 425 430

Thr Ser Asn Asp Ile Ile Val Glu Lys Val Asp Asn Ile Lys Gln Glu
435 440 445

Thr Asp Val Ala Lys Pro Lys Lys Asn Ser Asn Gln Gly Val Val Gly
450 455 460

Trp Val Lys Asp Lys Gly Leu Trp Tyr Tyr Leu Asn Glu Ser Gly Ser
465 470 475 480

Met Ala Thr Gly Trp Val Lys Asp Lys Gly Leu Trp Tyr Tyr Leu Asn
485 490 495

Glu Ser Gly Ser Met Ala Thr Gly Trp Val Lys Asp Lys Gly Leu Trp
500 505 510

Tyr Tyr Leu Asn Glu Ser Gly Ser Met Ala Thr Gly Trp Val Lys Asp
515 520 525

Lys Gly Leu Trp Tyr Tyr Leu Asn Glu Ser Gly Ser Met Ala Thr Gly
530 535 540

Trp Val Lys Asp Lys Gly Leu Trp Tyr Tyr Leu Asn Glu Ser Gly Ser
545 550 555 560

Met Ala Thr Gly Trp Val Lys Asp Lys Gly Leu Trp Tyr Tyr Leu Asn
565 570 575

Glu Ser Gly Ser Met Ala Thr Gly Trp Val Thr Val Ser Gly Lys Trp
580 585 590

Tyr Tyr Thr Tyr Asn Ser Gly Asp Leu Leu Val Asn Thr Thr Thr Pro
595 600 605

Asp Gly Tyr Arg Val Asn Ala Asn Gly Glu Trp Val Gly
610 615 620

<210> 237

<211> 626

<212> PRT

<213> Streptococcus pneumoniae

<400> 237

Met Val Arg Phe Thr Gly Leu Ser Leu Lys Gln Thr Gln Ala Ile Glu
1 5 10 15

Val Leu Lys Gly His Ile Ser Leu Pro Asp Val Glu Val Ala Val Thr
20 25 30

Gln Ser Asp Gln Ala Ser Ile Ser Ile Glu Gly Glu Glu Gly His Tyr
35 40 45

Gln Leu Thr Tyr Arg Lys Pro His Gln Leu Tyr Arg Ala Leu Ser Leu
50 55 60

Leu Val Thr Val Leu Ala Glu Ala Asp Lys Val Glu Ile Glu Glu Gln
65 70 75 80

Ala Ala Tyr Glu Asp Leu Ala Tyr Met Val Asp Cys Ser Arg Asn Ala
85 90 95

Val Leu Asn Val Ala Ser Ala Lys Gln Met Ile Glu Ile Leu Ala Leu
100 105 110

Met Gly Tyr Ser Thr Phe Glu Leu Tyr Met Glu Asp Thr Tyr Gln Ile
115 120 125

Glu Gly Gln Pro Tyr Phe Gly Tyr Phe Arg Gly Ala Tyr Ser Ala Glu
130 135 140

Glu Leu Gln Glu Ile Glu Ala Tyr Ala Gln Gln Phe Asp Val Thr Phe
145 150 155 160

Val Pro Cys Ile Gln Thr Leu Ala His Leu Ser Ala Phe Val Lys Trp
165 170 175

Gly Val Lys Glu Val Gln Glu Leu Arg Asp Val Glu Asp Ile Leu Leu
180 185 190

Ile Gly Glu Glu Lys Val Tyr Asp Leu Ile Asp Gly Met Phe Ala Thr
195 200 205

Leu Ser Lys Leu Lys Thr Arg Lys Val Asn Ile Gly Met Asp Glu Ala
210 215 220

His Leu Val Gly Leu Gly Arg Tyr Leu Ile Leu Asn Gly Val Val Asp
225 230 235 240

Arg Ser Leu Leu Met Cys Gln His Leu Glu Arg Val Leu Asp Ile Ala
245 250 255

Asp Lys Tyr Gly Phe His Cys Gln Met Trp Ser Asp Met Phe Phe Lys
260 265 270

Leu Met Ser Ala Asp Gly Gln Tyr Asp Arg Asp Val Glu Ile Pro Glu
275 280 285

Glu Thr Arg Val Tyr Leu Asp Arg Leu Lys Asp Arg Val Thr Leu Val
290 295 300

Tyr Trp Asp Tyr Tyr Gln Asp Ser Glu Glu Lys Tyr Asn Arg Asn Phe
305 310 315 320

Arg Asn His His Lys Ile Ser His Asp Leu Ala Phe Ala Gly Gly Ala
325 330 335

Trp Lys Trp Ile Gly Phe Thr Pro His Asn His Phe Ser Arg Leu Val
340 345 350

Ala Ile Glu Ala Asn Lys Ala Cys Arg Ala Asn Gln Ile Lys Glu Val
355 360 365

Ile Val Thr Gly Trp Gly Asp Asn Gly Gly Glu Thr Ala Gln Phe Ser
370 375 380

Ile Leu Pro Ser Leu Gln Ile Trp Ala Glu Leu Ser Tyr Arg Asn Asp
385 390 395 400

Leu Asp Gly Leu Ser Ala His Phe Lys Thr Asn Thr Gly Leu Thr Val
405 410 415

Glu Asp Phe Met Gln Ile Asp Leu Ala Asn Leu Leu Pro Asp Leu Pro
420 425 430

Gly Asn Leu Ser Gly Ile Asn Pro Asn Arg Tyr Val Phe Tyr Gln Asp
435 440 445

Ile Leu Cys Pro Ile Leu Asp Gln His Met Thr Pro Glu Gln Asp Lys
450 455 460

Pro His Phe Ala Gln Ala Ala Glu Thr Leu Ala Asn Ile Lys Glu Lys
465 470 475 480

Ala Gly Asn Tyr Ala Tyr Leu Phe Glu Thr Gln Ala Gln Leu Asn Ala
485 490 495

Ile Leu Ser Ser Lys Val Asp Val Gly Arg Arg Ile Arg Gln Ala Tyr
500 505 510

Gln Ala Asp Asp Lys Glu Ser Leu Gln Gln Ile Ala Arg Gln Glu Leu
515 520 525

Pro Glu Leu Arg Ser Gln Ile Glu Asp Phe His Ala Leu Phe Ser His
530 535 540

Gln Trp Leu Lys Glu Asn Lys Val Phe Gly Leu Asp Thr Val Asp Ile
545 550 555 560

Arg Met Gly Gly Leu Leu Gln Arg Ile Lys Arg Ala Glu Ser Arg Ile
565 570 575

Glu Val Tyr Leu Ala Gly Gln Leu Asp Arg Ile Asp Glu Leu Glu Val
580 585 590

Glu Ile Leu Pro Phe Thr Asp Phe Tyr Ala Asp Lys Asp Phe Ala Ala
595 600 605

Thr Thr Ala Asn Gln Trp His Thr Ile Ala Thr Ala Ser Thr Ile Tyr
610 615 620

Thr Thr
625

<210> 238

<211> 782

<212> PRT

<213> Streptococcus pneumoniae

<400> 238

Met Ser Asn Ser Phe Val Lys Leu Leu Val Ser Gln Leu Phe Ala Asn
1 5 10 15

Leu Ala Asp Ile Phe Phe Arg Val Thr Ile Ile Ala Asn Ile Tyr Ile
20 25 30

Ile Ser Lys Ser Val Ile Ala Thr Ser Leu Val Pro Ile Leu Ile Gly
35 40 45

Ile Ser Ser Phe Val Ala Ser Leu Leu Val Pro Leu Val Thr Lys Arg
50 55 60

Leu Ala Leu Asn Arg Val Leu Ser Leu Ser Gln Phe Gly Lys Thr Ile
65 70 75 80

Leu Leu Ala Ile Leu Val Gly Met Phe Thr Val Met Gln Ser Val Ala
85 90 95

Pro Leu Val Thr Tyr Leu Phe Val Val Ala Ile Ser Ile Leu Asp Gly
100 105 110

Phe Ala Ala Pro Val Ser Tyr Ala Ile Val Pro Arg Tyr Ala Thr Asp
115 120 125

Leu Gly Lys Ala Asn Ser Ala Leu Ser Met Thr Gly Glu Ala Val Gln
130 135 140

Leu Ile Gly Trp Gly Leu Gly Gly Leu Leu Phe Ala Thr Ile Gly Leu
145 150 155 160

Leu Pro Thr Thr Cys Ile Asn Leu Val Leu Tyr Ile Ile Ser Ser Phe
165 170 175

Leu Met Leu Phe Leu Pro Asn Ala Glu Val Glu Val Leu Glu Ser Glu
180 185 190

Thr Asn Leu Glu Ile Leu Leu Lys Gly Trp Lys Leu Val Ala Arg Asn
195 200 205

Pro Arg Leu Arg Leu Phe Val Ser Ala Asn Leu Leu Glu Ile Phe Ser
210 215 220

Asn Thr Ile Trp Val Ser Ser Ile Ile Leu Val Phe Val Thr Glu Leu
225 230 235 240

Leu Asn Lys Thr Glu Ser Tyr Trp Gly Tyr Ser Asn Thr Ala Tyr Ser
245 250 255

Ile Gly Ile Ile Ile Ser Gly Leu Ile Ala Phe Arg Leu Ser Glu Lys
260 265 270

Phe Leu Ala Ala Lys Trp Glu Pro Gln Leu Phe Thr Pro Asn Leu Lys
275 280 285

Thr Ile Gln Asn Pro Cys Leu Ser Leu Asp Pro Gly Trp Phe Leu Phe
290 295 300

Ser Pro Asn Gly Cys Phe Leu Leu Asp Lys Lys Glu Phe Pro Leu Tyr
305 310 315 320

Gly Ile Ser Val Glu Lys Asn Thr Lys Arg Lys Glu Thr His Met Asn
325 330 335

Ser Leu Pro Asn His His Phe Gln Asn Lys Ser Phe Tyr Gln Leu Ser
340 345 350

Phe Asp Gly Gly His Leu Thr Gln Tyr Gly Gly Leu Ile Phe Phe Gln
355 360 365

Glu Leu Phe Ser Gln Leu Lys Leu Lys Glu Arg Ile Ser Lys Tyr Leu
370 375 380

Val Thr Asn Asp Gln Arg Arg Tyr Cys Arg Tyr Ser Asp Ser Asp Ile
385 390 395 400

Leu Val Gln Phe Leu Phe Gln Leu Leu Thr Gly Tyr Gly Thr Asp Tyr
405 410 415

Ala Cys Lys Glu Leu Ser Ala Asp Ala Tyr Phe Pro Lys Leu Leu Glu
420 425 430

Gly Gly Gln Leu Ala Ser Gln Pro Thr Leu Ser Arg Phe Leu Ser Arg
435 440 445

Thr Asp Glu Glu Thr Val His Ser Leu Arg Cys Leu Asn Leu Glu Leu
450 455 460

Val Glu Phe Phe Leu Gln Phe His Gln Leu Asn Gln Leu Ile Val Asp
465 470 475 480

Ile Asp Ser Thr His Phe Thr Thr Tyr Gly Lys Gln Glu Gly Val Ala
485 490 495

Tyr Asn Ala His Tyr Arg Ala His Gly Tyr His Pro Leu Tyr Ala Phe
500 505 510

Glu Gly Lys Thr Gly Tyr Cys Phe Asn Ala Gln Leu Arg Pro Gly Asn
515 520 525

Arg Tyr Cys Ser Glu Glu Ala Asp Ser Phe Ile Thr Pro Val Leu Glu
530 535 540

Arg Phe Asn Gln Leu Leu Phe Arg Met Asp Ser Gly Phe Ala Thr Pro
545 550 555 560

Lys Leu Tyr Asp Leu Ile Glu Lys Thr Gly Gln Tyr Tyr Leu Ile Lys
565 570 575

Leu Lys Lys Asn Thr Val Leu Ser Arg Leu Gly Asp Leu Ser Leu Pro
580 585 590

Cys Pro Gln Asp Glu Asp Leu Thr Ile Leu Pro His Ser Ala Tyr Ser
595 600 605

Glu Thr Leu Tyr Gln Ala Gly Ser Trp Ser His Lys Arg Arg Val Cys
610 615 620

Gln Phe Ser Glu Arg Lys Glu Gly Asn Leu Phe Tyr Asp Val Ile Ser
625 630 635 640

Leu Val Thr Asn Met Thr Ser Gly Thr Ser Gln Asp Gln Phe Gln Leu
645 650 655

Tyr Arg Gly Arg Gly Gln Ala Glu Asn Phe Ile Lys Glu Met Lys Glu
660 665 670

Gly Phe Phe Gly Asp Lys Thr Asp Ser Ser Thr Leu Ile Lys Asn Glu
675 680 685

Val Arg Met Met Met Ser Cys Ile Ala Tyr Asn Leu Tyr Leu Phe Leu
690 695 700

Lys His Leu Ala Gly Gly Asp Phe Gln Thr Leu Thr Ile Lys Arg Phe
705 710 715 720

Arg His Leu Phe Leu His Val Val Gly Lys Cys Val Arg Thr Gly Arg
725 730 735

Lys Gln Leu Leu Lys Leu Ser Ser Leu Tyr Ala Tyr Ser Glu Leu Phe
740 745 750

Ser Ala Leu Tyr Ser Arg Ile Arg Lys Val Asn Leu Asn Leu Pro Val
755 760 765

Pro Tyr Glu Pro Pro Arg Arg Lys Ala Ser Leu Met Met His
770 775 780

<210> 239

<211> 693

<212> PRT

<213> Streptococcus pneumoniae

<400> 239

Met Phe Ala Ser Lys Ser Glu Arg Lys Val His Tyr Ser Ile Arg Lys
1 5 10 15

Phe Ser Val Gly Val Ala Ser Val Val Val Ala Ser Leu Val Met Gly
20 25 30

Ser Val Val His Ala Thr Glu Asn Glu Gly Ala Thr Gln Val Pro Thr
35 40 45

Ser Ser Asn Arg Ala Asn Glu Ser Gln Ala Glu Gln Gly Glu Gln Pro
50 55 60

Lys Lys Leu Asp Ser Glu Arg Asp Lys Ala Arg Lys Glu Val Glu Glu
65 70 75 80

Tyr Val Lys Lys Ile Val Gly Glu Ser Tyr Ala Lys Ser Thr Lys Lys
85 90 95

Arg His Thr Ile Thr Val Ala Leu Val Asn Glu Leu Asn Asn Ile Lys
100 105 110

Asn Glu Tyr Leu Asn Lys Ile Val Glu Ser Thr Ser Glu Ser Gln Leu
115 120 125

Gln Ile Leu Met Met Glu Ser Arg Ser Lys Val Asp Glu Ala Val Ser
130 135 140

Lys Phe Glu Lys Asp Ser Ser Ser Ser Ser Ser Ser Asp Ser Ser Thr
145 150 155 160

Lys Pro Glu Ala Ser Asp Thr Ala Lys Pro Asn Lys Pro Thr Glu Pro
165 170 175

Gly Glu Lys Val Ala Glu Ala Lys Lys Lys Val Glu Glu Ala Glu Lys
180 185 190

Lys Ala Lys Asp Gln Lys Glu Glu Asp Arg Arg Asn Tyr Pro Thr Ile
195 200 205

Thr Tyr Lys Thr Leu Glu Leu Glu Ile Ala Glu Ser Asp Val Glu Val
210 215 220

Lys Lys Ala Glu Leu Glu Leu Val Lys Val Lys Ala Asn Glu Pro Arg
225 230 235 240

Asp Glu Gln Lys Ile Lys Gln Ala Glu Ala Glu Val Glu Ser Lys Gln
245 250 255

Ala Glu Ala Thr Arg Leu Lys Lys Ile Lys Thr Asp Arg Glu Glu Ala
260 265 270

Glu Glu Glu Ala Lys Arg Arg Ala Asp Ala Lys Glu Gln Gly Lys Pro
275 280 285

Lys Gly Arg Ala Lys Arg Gly Val Pro Gly Glu Leu Ala Thr Pro Asp
290 295 300

Lys Lys Glu Asn Asp Ala Lys Ser Ser Asp Ser Ser Val Gly Glu Glu
305 310 315 320

Thr Leu Pro Ser Pro Ser Leu Lys Pro Glu Lys Lys Val Ala Glu Ala
325 330 335

Glu Lys Lys Val Glu Glu Ala Lys Lys Lys Ala Glu Asp Gln Lys Glu
340 345 350

Glu Asp Arg Arg Asn Tyr Pro Thr Asn Thr Tyr Lys Thr Leu Glu Leu
355 360 365

Glu Ile Ala Glu Ser Asp Val Glu Val Lys Lys Ala Glu Leu Glu Leu
370 375 380

Val Lys Glu Glu Ala Lys Glu Pro Arg Asn Glu Glu Lys Val Lys Gln
385 390 395 400

Ala Lys Ala Glu Val Glu Ser Lys Lys Ala Glu Ala Thr Arg Leu Glu
405 410 415

Lys Ile Lys Thr Asp Arg Lys Lys Ala Glu Glu Glu Ala Lys Arg Lys
420 425 430

Ala Ala Glu Glu Asp Lys Val Lys Glu Lys Pro Ala Glu Gln Pro Gln
435 440 445

Pro Ala Pro Ala Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro Lys Pro
450 455 460

Glu Asn Pro Ala Glu Gln Pro Lys Ala Glu Lys Pro Ala Asp Gln Gln
465 470 475 480

Ala Glu Glu Asp Tyr Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg Leu
485 490 495

Thr Gln Gln Gln Pro Pro Lys Thr Glu Lys Pro Ala Gln Pro Ser Thr
500 505 510

Pro Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn
515 520 525

Thr Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp
530 535 540

Tyr Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Asn
545 550 555 560

Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser Met Ala Thr Gly
565 570 575

Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ser
580 585 590

Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn
595 600 605

Ala Asn Gly Ser Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp
610 615 620

Tyr Tyr Leu Asn Ala Asn Gly Asp Met Ala Thr Gly Trp Val Lys Asp
625 630 635 640

Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala Ser
645 650 655

Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Ser Gly
660 665 670

Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Gly Val Asn Ala Asn
675 680 685

Gly Glu Trp Val Asn
690

<210> 240

<211> 810

<212> PRT

<213> Streptococcus pneumoniae

<400> 240

Met Asn Tyr Ser Lys Ala Leu Asn Glu Cys Ile Glu Ser Ala Tyr Met
1 5 10 15

Val Ala Gly His Phe Gly Ala Arg Tyr Leu Glu Ser Trp His Leu Leu
20 25 30

Ile Ala Met Ser Asn His Ser Tyr Ser Val Ala Gly Ala Thr Leu Asn
35 40 45

Asp Tyr Pro Tyr Glu Met Asp Arg Leu Glu Glu Val Ala Leu Glu Leu
50 55 60

Thr Glu Thr Asp Tyr Ser Gln Asp Glu Thr Phe Thr Glu Leu Pro Phe
65 70 75 80

Ser Arg Arg Leu Gln Val Leu Phe Asp Glu Ala Glu Tyr Val Ala Ser
85 90 95

Val Val His Ala Lys Val Leu Gly Thr Glu His Val Leu Tyr Ala Ile
100 105 110

Leu His Asp Ser Asn Ala Leu Ala Thr Arg Ile Leu Glu Arg Ala Gly
115 120 125

Phe Ser Tyr Glu Asp Lys Lys Asp Gln Val Lys Ile Ala Ala Leu Arg
130 135 140

Arg Asn Leu Glu Glu Arg Ala Gly Trp Thr Arg Glu Asp Leu Lys Ala
145 150 155 160

Leu Arg Gln Arg His Arg Thr Val Ala Asp Lys Gln Asn Ser Met Ala
165 170 175

Asn Met Met Gly Met Pro Gln Thr Pro Ser Gly Gly Leu Glu Asp Tyr
180 185 190

Thr His Asp Leu Thr Glu Gln Ala Arg Ser Gly Lys Leu Glu Pro Val
195 200 205

Ile Gly Arg Asp Lys Glu Ile Ser Arg Met Ile Gln Ile Leu Ser Arg
210 215 220

Lys Thr Lys Asn Asn Pro Val Leu Val Gly Asp Ala Gly Val Gly Lys
225 230 235 240

Thr Ala Leu Ala Leu Gly Leu Ala Gln Arg Ile Ala Ser Gly Asp Val
245 250 255

Pro Ala Glu Met Ala Lys Met Arg Val Leu Glu Leu Asp Leu Met Asn
260 265 270

Val Val Ala Gly Thr Arg Phe Arg Gly Asp Phe Glu Glu Arg Met Asn
275 280 285

Asn Ile Ile Lys Asp Ile Glu Glu Asp Gly Gln Val Ile Leu Phe Ile
290 295 300

Asp Glu Leu His Thr Ile Met Gly Ser Gly Ser Gly Ile Asp Ser Thr
305 310 315 320

Leu Asp Ala Ala Asn Ile Leu Lys Pro Ala Leu Ala Arg Gly Thr Leu
325 330 335

Arg Thr Val Gly Ala Thr Thr Gln Glu Glu Tyr Gln Lys His Ile Glu
340 345 350

Lys Asp Ala Ala Leu Ser Arg Arg Phe Ala Lys Val Thr Ile Glu Glu
355 360 365

Pro Ser Val Ala Asp Ser Met Thr Ile Leu Gln Gly Leu Lys Ala Thr
370 375 380

Tyr Glu Lys His His Arg Val Gln Ile Thr Asp Glu Ala Val Glu Thr
385 390 395 400

Ala Val Lys Met Ala His Arg Tyr Leu Thr Ser Arg His Leu Pro Asp
405 410 415

Ser Ala Ile Asp Leu Leu Asp Glu Ala Ala Ala Thr Val Gln Asn Lys
420 425 430

Ala Lys His Val Lys Ala Asp Asp Ser Asp Leu Ser Pro Ala Asp Lys
435 440 445

Ala Leu Met Asp Gly Lys Trp Lys Gln Ala Ala Gln Leu Ile Ala Lys
450 455 460

Glu Glu Glu Val Pro Val Tyr Lys Asp Leu Val Thr Glu Ser Asp Ile
465 470 475 480

Leu Thr Thr Leu Ser Arg Leu Ser Gly Ile Pro Val Gln Lys Leu Thr
485 490 495

Gln Thr Asp Ala Lys Lys Tyr Leu Asn Leu Glu Ala Glu Leu His Lys
500 505 510

Arg Val Ile Gly Gln Asp Gln Ala Val Ser Ser Ile Ser Arg Ala Ile
515 520 525

Arg Arg Asn Gln Ser Gly Ile Arg Ser His Lys Arg Pro Ile Gly Ser
530 535 540

Phe Met Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Glu Leu Ala Lys
545 550 555 560

Ala Leu Ala Glu Val Leu Phe Asp Asp Glu Ser Ala Leu Ile Arg Phe
565 570 575

Asp Met Ser Glu Tyr Met Glu Lys Phe Ala Ala Ser Arg Leu Asn Gly
580 585 590

Ala Pro Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Glu Leu Thr Glu
595 600 605

Lys Val Arg Asn Lys Pro Tyr Ser Val Leu Leu Phe Asp Glu Val Glu
610 615 620

Lys Ala His Pro Asp Ile Phe Asn Val Leu Leu Gln Val Leu Asp Asp
625 630 635 640

Gly Val Leu Thr Asp Ser Lys Gly Arg Lys Val Asp Phe Ser Asn Thr
645 650 655

Ile Ile Ile Met Thr Ser Asn Leu Gly Ala Thr Ala Leu Arg Asp Asp
660 665 670

Lys Thr Val Gly Phe Gly Ala Lys Asp Ile Arg Phe Asp Gln Glu Asn
675 680 685

Met Glu Lys Arg Met Phe Glu Glu Leu Lys Lys Ala Tyr Arg Pro Glu
690 695 700

Phe Ile Asn Arg Ile Asp Glu Lys Val Val Phe His Ser Leu Ser Ser
705 710 715 720

Asp His Met Gln Glu Val Val Lys Ile Met Val Lys Pro Leu Val Ala
725 730 735

Ser Leu Thr Glu Lys Gly Ile Asp Leu Lys Leu Gln Ala Ser Ala Leu
740 745 750

Lys Leu Leu Ala Asn Gln Gly Tyr Asp Pro Glu Met Gly Ala Arg Pro
755 760 765

Leu Arg Arg Thr Leu Gln Thr Glu Val Glu Asp Lys Leu Ala Glu Leu
770 775 780

Leu Leu Lys Gly Asp Leu Val Ala Gly Ser Thr Leu Lys Ile Gly Val
785 790 795 800

Lys Ala Gly Gln Leu Lys Phe Asp Ile Ala
805 810

<210> 241

<211> 448

<212> PRT

<213> Streptococcus pneumoniae

<400> 241

Met Lys Ile Leu Pro Phe Ile Ala Arg Gly Thr Ser Tyr Tyr Leu Lys
1 5 10 15

Met Ser Val Lys Lys Leu Val Pro Phe Leu Val Val Gly Leu Met Leu
20 25 30

Ala Ala Gly Asp Ser Val Tyr Ala Tyr Ser Arg Gly Asn Gly Ser Ile
35 40 45

Ala Arg Gly Asp Asp Tyr Pro Ala Tyr Tyr Lys Asn Gly Ser Gln Glu
50 55 60

Ile Asp Gln Trp Arg Met Tyr Ser Arg Gln Cys Thr Ser Phe Val Ala
65 70 75 80

Phe Arg Leu Ser Asn Val Asn Gly Phe Glu Ile Pro Ala Ala Tyr Gly
85 90 95

Asn Ala Asn Glu Trp Gly His Arg Ala Arg Arg Glu Gly Tyr Arg Val
100 105 110

Asp Asn Thr Pro Thr Ile Gly Ser Ile Thr Trp Ser Thr Ala Gly Thr
115 120 125

Tyr Gly His Val Ala Trp Val Ser Asn Val Met Gly Asp Gln Ile Glu
130 135 140

Ile Glu Glu Tyr Asn Tyr Gly Tyr Thr Glu Ser Tyr Asn Lys Arg Val
145 150 155 160

Ile Lys Ala Asn Thr Met Thr Gly Phe Ile His Phe Lys Asp Leu Asp
165 170 175

Gly Gly Ser Val Gly Asn Ser Gln Ser Ser Thr Ser Thr Gly Gly Thr
180 185 190

His Tyr Phe Lys Thr Lys Ser Ala Ile Lys Thr Glu Pro Leu Ala Ser
195 200 205

Gly Thr Val Ile Asp Tyr Tyr Tyr Pro Gly Glu Lys Val His Tyr Asp
210 215 220

Gln Ile Leu Glu Lys Asp Gly Tyr Lys Trp Leu Ser Tyr Thr Ala Tyr
225 230 235 240

Asn Gly Ser Tyr Arg Tyr Val Gln Leu Glu Ala Val Asn Lys Asn Pro
245 250 255

Leu Gly Asn Ser Val Leu Ser Ser Thr Gly Gly Thr His Tyr Phe Lys
260 265 270

Thr Lys Ser Ala Ile Lys Thr Glu Pro Leu Val Ser Ala Thr Val Ile
275 280 285

Asp Tyr Tyr Tyr Pro Gly Glu Lys Val His Tyr Asp Gln Ile Leu Glu
290 295 300

Lys Asp Gly Tyr Lys Trp Leu Ser Tyr Thr Ala Tyr Asn Gly Ser Arg
305 310 315 320

Arg Tyr Ile Gln Leu Glu Gly Val Thr Ser Ser Gln Asn Tyr Gln Asn
325 330 335

Gln Ser Gly Asn Ile Ser Ser Tyr Gly Ser His Ser Ser Ser Thr Val
340 345 350

Gly Trp Lys Lys Ile Asn Gly Ser Trp Tyr His Phe Lys Ser Asn Gly
355 360 365

Ser Lys Ser Thr Gly Trp Leu Lys Asp Gly Ser Ser Trp Tyr Tyr Leu
370 375 380

Lys Leu Ser Gly Glu Met Gln Thr Gly Trp Leu Lys Glu Asn Gly Leu
385 390 395 400

Trp Tyr Tyr Leu Gly Ser Ser Gly Ala Met Lys Thr Gly Trp Tyr Gln
405 410 415

Val Ser Gly Lys Trp Tyr Tyr Ser Tyr Ser Ser Gly Ala Leu Ala Val
420 425 430

Asn Thr Thr Val Asp Gly Tyr Arg Val Asn Ser Asp Gly Glu Arg Val
435 440 445

<210> 242

<211> 150

<212> PRT

<213> Streptococcus pneumoniae

<400> 242

Met Lys Val Ile Phe Leu Ala Asp Val Lys Gly Lys Gly Lys Lys Gly
1 5 10 15

Glu Ile Lys Glu Val Pro Thr Gly Tyr Ala Gln Asn Phe Leu Ile Lys
20 25 30

Lys Asn Leu Ala Lys Glu Ala Thr Ala Gln Ala Val Gly Glu Leu Arg
35 40 45

Gly Lys Gln Lys Ser Glu Glu Lys Ala His Ala Glu Met Ile Ala Glu
50 55 60

Gly Lys Ala Ile Lys Ala Gln Leu Glu Ala Glu Glu Thr Val Val Glu
65 70 75 80

Phe Val Glu Lys Val Gly Pro Asp Gly Arg Thr Phe Gly Ser Ile Thr
85 90 95

Asn Lys Lys Ile Ala Glu Glu Leu Gln Lys Gln Phe Gly Ile Lys Ile
100 105 110

Asp Lys Arg His Ile Gln Val Gln Ala Pro Ile Arg Ala Val Gly Leu
115 120 125

Ile Asp Val Pro Val Lys Ile Tyr Gln Asp Ile Thr Ser Val Ile Asn
130 135 140

Leu Arg Val Lys Glu Gly
145 150

<210> 243

<211> 392

<212> PRT

<213> Streptococcus pneumoniae

<400> 243

Met Lys Lys Lys Ile Leu Ala Ser Leu Leu Leu Ser Thr Val Met Val
1 5 10 15

Ser Gln Val Ala Val Leu Thr Thr Ala His Ala Glu Thr Thr Asp Asp
20 25 30

Lys Ile Ala Ala Gln Asp Asn Lys Ile Ser Asn Leu Thr Ala Gln Gln
35 40 45

Gln Glu Ala Gln Lys Gln Val Asp Gln Ile Gln Glu Gln Val Ser Ala
50 55 60

Ile Gln Ala Glu Gln Ser Asn Leu Gln Ala Glu Asn Asp Arg Leu Gln
65 70 75 80

Ala Glu Ser Lys Lys Leu Glu Gly Glu Ile Thr Glu Leu Ser Lys Asn
85 90 95

Ile Val Ser Arg Asn Gln Ser Leu Glu Lys Gln Ala Arg Ser Ala Gln
100 105 110

Thr Asn Gly Ala Val Thr Ser Tyr Ile Asn Thr Ile Val Asn Ser Lys
115 120 125

Ser Ile Thr Glu Ala Ile Ser Arg Val Ala Ala Met Ser Glu Ile Val
130 135 140

Ser Ala Asn Asn Lys Met Leu Glu Gln Gln Lys Ala Asp Lys Lys Ala
145 150 155 160

Ile Ser Glu Lys Gln Val Ala Asn Asn Asp Ala Ile Asn Thr Val Ile
165 170 175

Ala Asn Gln Gln Lys Leu Ala Asp Asp Ala Gln Ala Leu Thr Thr Lys
180 185 190

Gln Ala Glu Leu Lys Ala Ala Glu Leu Ser Leu Ala Ala Glu Lys Ala
195 200 205

Thr Ala Glu Gly Glu Lys Ala Ser Leu Leu Glu Gln Lys Ala Ala Ala
210 215 220

Glu Ala Glu Ala Arg Ala Ala Ala Val Ala Glu Ala Ala Tyr Lys Glu
225 230 235 240

Lys Arg Ala Ser Gln Gln Gln Ser Val Leu Ala Ser Ala Asn Thr Asn
245 250 255

Leu Thr Ala Gln Val Gln Ala Val Ser Glu Ser Ala Ala Ala Pro Val
260 265 270

Arg Ala Lys Val Arg Pro Thr Tyr Ser Thr Asn Ala Ser Ser Tyr Pro
275 280 285

Ile Gly Glu Cys Thr Trp Gly Val Lys Thr Leu Ala Pro Trp Ala Gly
290 295 300

Asp Tyr Trp Gly Asn Gly Ala Gln Trp Ala Thr Ser Ala Ala Ala Ala
305 310 315 320

Gly Phe Arg Thr Gly Ser Thr Pro Gln Val Gly Ala Ile Ala Cys Trp
325 330 335

Asn Asp Gly Gly Tyr Gly His Val Ala Val Val Thr Ala Val Glu Ser
340 345 350

Thr Thr Arg Ile Gln Val Ser Glu Ser Asn Tyr Ala Gly Asn Arg Thr
355 360 365

Ile Gly Asn His Arg Gly Trp Phe Asn Pro Thr Thr Thr Ser Glu Gly
370 375 380

Phe Val Thr Tyr Ile Tyr Ala Asp
385 390

<210> 244

<211> 129

<212> PRT

<213> Streptococcus pneumoniae

<400> 244

Met Val Lys Arg Arg Ile Arg Arg Gly Thr Arg Glu Pro Glu Lys Val
1 5 10 15

Val Val Pro Glu Gln Ser Ser Ile Pro Ser Tyr Pro Val Ser Val Thr
20 25 30

Ser Asn Gln Gly Thr Asp Val Ala Val Glu Pro Ala Lys Ala Val Ala
35 40 45

Pro Thr Thr Asp Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn
50 55 60

Thr Asp Gly Ser Met Ala Thr Gly Trp Val Gln Val Asn Ser Ser Trp
65 70 75 80

Tyr Tyr Leu Asn Ser Asn Gly Ser Met Lys Val Asn Gln Trp Phe Gln
85 90 95

Val Gly Gly Lys Trp Tyr Tyr Val Asn Thr Ser Gly Glu Leu Ala Val
100 105 110

Asn Thr Ser Ile Asp Gly Tyr Arg Val Asn Asp Asn Gly Glu Trp Val
115 120 125

Arg

<210> 245

<211> 46

<212> PRT

<213> Streptococcus pneumoniae

<400> 245

Glu Leu Arg Arg Leu Ser Arg Leu Val Asp Gln Glu Leu Tyr Phe Gly
1 5 10 15

Cys Gly Trp Arg Leu Ser Leu Glu Trp Leu Pro Ser Met Arg Lys Asp
20 25 30

Ser Trp Pro Ser Asn Thr Ala Pro Arg Thr Thr Met Val Gln
35 40 45

<210> 246

<211> 31

<212> PRT

<213> Streptococcus pneumoniae

<400> 246

Asp Cys Ile Arg Lys Gln Pro Phe Thr Arg Asp Glu Pro Asn Lys Thr
1   5   10   15

Cys Arg Lys Thr Lys Pro Ser Lys Ser Tyr Cys Ser Tyr Arg Trp
            20   25   30

<210> 247

<211> 26

<212> PRT

<213> Streptococcus pneumoniae

<400> 247

Gly Gln Arg Asn Pro Arg Arg Ile Glu Arg Val Ile Arg Met Ala Glu
1   5   10   15

Thr Lys Pro Arg Ile Ser Lys Lys Glu Gly
            20   25

<210> 248

<211> 83

<212> PRT

<213> Streptococcus pneumoniae

<400> 248

Gln Arg Lys Leu Phe Lys Ile Phe His Leu Phe Gln Lys Lys Ser Gly
1   5   10   15

Trp Asn Gln Lys Ser Ser Cys Leu Lys Leu Asn Leu Asn Ser Leu Asn
            20   25   30

Arg Lys Met Thr Gln Met Thr Lys Met Phe Arg Ser Ile Phe Gln Pro
        35   40   45

Lys Lys Pro Leu Asn Thr Asn Phe Gln Ala Tyr Asn Ser Leu His Gln
    50   55   60

Ile Asn Gln Lys Ile Ser Leu Lys Arg Arg Lys Leu Ser Glu Lys Ile
65   70   75   80

Ser Lys Ser

<210> 249

<211> 104

<212> PRT

<213> Streptococcus pneumoniae

<400> 249

Leu Val Ile Ile Val Leu Lys Ile Gln Ser Lys Ser Glu Thr Asp Phe
1   5   10   15

Ile Phe Lys Thr Trp Pro Phe Ile Leu Leu Ser Lys Ile Ile Pro Leu
            20   25   30

Met Val Leu Asp Cys Gln Val Ser Ile Ser Trp Thr Asn Arg Glu Thr
        35   40   45

Val Ala Tyr Ser Lys Leu Leu Ala Ile Lys Thr Leu Lys Gly Asp Tyr
    50   55   60

His Asp Gly Gln Ser Lys Lys Ile Arg Leu Ser His Ala Ser Arg Val
65   70   75   80

Arg Thr Pro Ser Trp Tyr Pro His Asp Met Ala Asp Ser Thr Arg Ile
                85   90   95

Met Ala Phe Ser Arg Lys Gly Cys
            100

<210> 250

<211> 30

<212> PRT

<213> Streptococcus pneumoniae

<400> 250

Glu Arg Leu Pro Ala Phe Pro Arg Ser Leu Ser Gly Arg Lys Leu Asp
1   5   10   15

Gln Gly Gly Thr Lys Glu Lys Gly Ser Asp Gly Arg Ser Pro
            20   25   30

<210> 251

<211> 245

<212> PRT

<213> Streptococcus pneumoniae

<400> 251

Arg Asn Cys Leu Ser Thr Trp Lys Ser Ser Ser Asn Tyr His Thr Glu
1   5   10   15

Ile Lys Arg Gly Thr Val Arg Gln Cys Leu Gly Lys Gly Arg Phe Lys
            20   25   30

Glu Val Tyr Ser Ala Asp Tyr Ala Gln Gln Ser Tyr Glu Asn Asn Arg
        35   40   45

Lys Arg Ser Val Lys Lys Ser Ser Leu Thr Lys Glu Leu Lys Glu Lys
    50   55   60

Ile Leu His Tyr His Asn Gln Lys Phe Ser Pro Glu Met Met Val Met
65   70   75   80

Ala Lys Gly Val Asn Val Gly Ile Ser Thr Ile Tyr Tyr Trp Ile His
                85   90   95

His Gly Lys Leu Gly Leu Ser Lys Gln Asp Leu Leu Tyr Pro Arg Lys
            100   105   110

Gly Lys Ala Leu Lys Lys Gln Ala Ser Thr Asn Phe Lys Pro Ala Gly
        115   120   125

Gln Ser Ile Glu Gln Arg Pro Glu Ala Ile Asn Leu Arg Leu Glu Asn
    130   135   140

Gly His Tyr Glu Ile Asp Thr Val Leu Leu Thr Arg Ser Lys Asn Tyr
145   150   155   160

Cys Leu Ile Val Leu Thr Asp Arg Lys Ser Arg His Gln Ile Ile Arg
                165   170   175

Leu Ile Pro Asn Lys Ser Ala Glu Val Val Asn Gln Ala Leu Lys Leu
            180   185   190

Ile Leu Lys Gln His Lys Ile Leu Ser Ile Thr Ala Asp Asn Gly Thr
        195   200   205

Glu Phe Asn Arg Leu Phe Asp Ile Phe Ser Glu Glu His Ile Tyr Tyr
    210   215   220

Ala His Pro Tyr Ala Ser Trp Glu Arg Gly Thr Asn Glu Asn His Asn
225   230   235   240

Arg Leu Ile Arg Arg
                245

<210> 252

<211> 36

<212> PRT

<213> Streptococcus pneumoniae

<400> 252

Pro Val Met Thr Ile Ser Ser Pro Thr Met Lys Asn Met Asp Leu Ser
1 5 10 15

Thr Lys Ala Ser Pro Ser Gln Pro Leu Gln Gly Lys His Gly Met Ile
20 25 30

Trp Ser Gly Lys
35

<210> 253

<211> 28

<212> PRT

<213> Streptococcus pneumoniae

<400> 253

Thr Ser Ser Ile Arg Ile His Thr Arg Lys Ser Ser Pro Asn Trp Thr
1 5 10 15

Thr Thr Pro His Leu Ala Leu Ser Ala Glu Thr Asn
20 25

<210> 254

<211> 27

<212> PRT

<213> Streptococcus pneumoniae

<400> 254

Tyr Phe Leu Pro His Lys Tyr Ala Arg Glu Ser Leu Ser Leu Pro Ser
1 5 10 15

Thr Asn Lys Ile Leu His Arg Lys Gln Gly Ser
20 25

<210> 255

<211> 53

<212> PRT

<213> Streptococcus pneumoniae

<400> 255

Ala Ala Phe Lys Lys Asp Gln Ile Asn Glu Arg Val Glu Lys Leu Gly
1 5 10 15

Lys Leu Lys Pro Ile Thr Ile Asn Tyr Asn Gly Lys Ser Glu Val Ile
20 25 30

Asp Ser Lys Glu Lys Leu Gln Glu Leu Met Asn Lys Ala Val Lys Asp
35 40 45

Glu Val Ala Gln Ile
50

<210> 256

<211> 33

<212> PRT

<213> Streptococcus pneumoniae

<400> 256

Ala Tyr Ala His Ser Lys Arg Ser Ala Gly Ser Gly Arg Ala Gly Gly
1 5 10 15

Arg Gln Cys Leu Cys Gln Cys Gln Asn Lys Cys Arg Arg Asp Phe Lys
20 25 30

Tyr

<210> 257

<211> 36

<212> PRT

<213> Streptococcus pneumoniae

<400> 257

His Gly Arg Pro Tyr His Lys Pro His Gln Pro His His His Gly Phe
1 5 10 15

Pro Gln Gln Ser Tyr Asn Leu Leu Pro Pro Lys His Lys Pro Thr Leu
20 25 30

Cys Val Arg Arg
        35

<210> 258

<211> 130

<212> PRT

<213> Streptococcus pneumoniae

<400> 258

Lys Gly Lys Ile Leu Leu Leu Pro Arg Leu Thr Thr Gln Arg Trp Gln
1   5   10   15

Arg Lys Ile Arg Pro Asp Ser Arg Lys Ser Ala Asn Asn Lys Ala Asn
            20   25   30

Leu Asp Phe His Asn Ser Arg Cys Lys Ser Ser Leu Ser Asp Glu Ala
        35   40   45

Pro Asn Leu His Lys Asn Pro Ala Leu Leu Val His Ser Leu Ser Arg
    50   55   60

Val Ile Ala Val Leu Leu Glu Leu Ser Pro Leu Gln Ala Tyr Ser Ile
65   70   75   80

Val Lys Phe Ser Pro Lys Glu Asp Asp Leu Ile His Asp Asp Ala Ile
                85   90   95

Leu Val Arg Phe Gly Ile Leu Glu Val His Asp Ser Pro Tyr Glu Leu
            100   105   110

Leu Leu Leu Tyr His Thr His Ser Tyr Arg Phe Ser Cys Ser Ile Tyr
        115   120   125

Leu Ser
    130

<210> 259

<211> 144

<212> PRT

<213> Streptococcus pneumoniae

<400> 259

Phe Thr Val Ser His Val Phe Leu Leu Tyr Leu Ser Phe Asn Pro Arg
1   5   10   15

Pro Lys Ser Met Ser Leu Ser Phe Thr Ser Ser Lys Leu Leu Arg Pro
20 25 30

Arg Phe Arg Thr Phe Ile Ile Ser Ala Ser Asp Phe Ser Val Lys Ser
35 40 45

Cys Thr Val Leu Ile Pro Ala Arg Phe Lys Gln Leu Tyr Glu Arg Thr
50 55 60

Asp Lys Ser Ser Ser Ser Ile Val Arg Ser Lys Ile Arg Ser Ser Asp
65 70 75 80

Ser Val Ser Ala Ser Phe Ile Thr Ser Val Asp Leu Ala Ile Ser Val
85 90 95

Arg Phe Val Asn Lys Ser Arg Cys Ser Val Lys Ile Arg Ala Glu Ser
100 105 110

Pro Lys Ala Ser Ser Gly Ile Ile Val Pro Phe Val Lys Ile Ser Arg
115 120 125

Val Asn Leu Ser Lys Pro Ser Leu Leu Pro Thr Arg Ala Gly Ser Thr
130 135 140

<210> 260

<211> 18

<212> PRT

<213> Streptococcus pneumoniae

<400> 260

Leu Val Cys Met Lys Asn Lys Gly Cys Tyr Lys Glu Arg Asn Asn Cys
1 5 10 15

Cys His

<210> 261

<211> 58

<212> PRT

<213> Streptococcus pneumoniae

<400> 261

Phe His Tyr Leu Ser Lys Tyr Phe Leu Val Ser Ala Ile Thr Thr Gly
1 5 10 15

```
Asp Lys Thr Lys Arg Ala Ile Lys Phe Gly Arg Ala Ile Lys Ala Leu
            20                  25                  30

Thr Ile Ser Ala Ile Ile Gln Thr Ile Ser Asn Ser Ile Asn Pro Pro
        35                  40                  45

Asn Lys Thr Met Ser Thr Lys Thr Thr Arg
    50                  55
```

<210> 262

<211> 47

<212> PRT

<213> Streptococcus pneumoniae

<400> 262

```
Gly Lys Lys Val Phe Ile Lys Tyr Pro Leu Ser Arg Val Ser Ser Lys
1               5                   10                  15

Thr Gly Pro Met Ile Thr Gly Arg Thr Lys Asp Lys Ile Val Asp Lys
            20                  25                  30

Lys Val Gly Cys Pro Phe Glu Lys Ser Thr Val Lys Tyr Ser Ser
        35                  40                  45
```

<210> 263

<211> 37

<212> PRT

<213> Streptococcus pneumoniae

<400> 263

```
Ser Ser Pro Val Phe Pro Lys Leu Val Met Val Ser Gly Ala Asn Lys
1               5                   10                  15

Pro Arg Glu Arg Arg Asn Phe Pro Phe Ser Ser Lys Met Ser Phe His
            20                  25                  30

Leu Thr Phe Val Leu
        35
```

<210> 264

<211> 77

<212> PRT

<213> Streptococcus pneumoniae

<400> 264

Tyr Leu Thr Ser Phe Ser Val Pro Lys Ile Ala Ser Ser Lys Val Lys
1   5   10   15

Leu Thr Arg Tyr Trp Arg Ser Ser Pro Trp Arg Gly Ala Phe Gly Leu
            20   25   30

Arg Glu Glu Pro Pro Pro Pro Lys Lys Leu Glu Lys Ile Ser Ser Lys
        35   40   45

Pro Pro Lys Pro Pro Ala Pro Leu Lys Pro Pro Lys Pro Pro Ala Pro
    50   55   60

Pro Lys Pro Pro Leu Ala Pro Ala Ala Pro Tyr Trp Ser
65   70   75

<210> 265

<211> 89

<212> PRT

<213> Streptococcus pneumoniae

<400> 265

Gln Ser Trp Arg Pro Ile Pro Asp Ser Lys Cys Tyr Thr Gln Glu Lys
1   5   10   15

Leu Thr Ile Pro Ile Lys Arg Arg Lys Asp Ile Lys Asp Phe Tyr His
            20   25   30

Asn Ser Ile Gln Arg His Lys Asn Ser His Lys Ser His Leu Leu Asp
        35   40   45

Ser Tyr Arg Leu Ile Ile Thr Arg Leu Ala Glu Ile Val His Glu Asn
    50   55   60

Lys Ile Leu Ile Val Leu Ile Leu Tyr Val Thr Asn Ile Pro Ser Arg
65   70   75   80

Ser Arg Arg Tyr Glu Val Asn Arg Val
                85

<210> 266

<211> 60

<212> PRT

<213> Streptococcus pneumoniae

<400> 266

Leu Phe Arg Phe Tyr Arg Val Ile Val Leu Tyr Arg Gly Trp His Ile
1   5   10   15

Tyr Leu Leu Ile Leu Val Asn Leu Gln Tyr Val Gln Asn Val Phe Arg
            20   25   30

Lys Asp Arg Phe Leu Val Arg Gly Ala Gln Pro Phe Phe His Gly Glu
        35   40   45

Arg Ser Ala Gly His Leu Val Leu Pro Tyr Val Leu
    50   55   60

<210> 267

<211> 60

<212> PRT

<213> Streptococcus pneumoniae

<400> 267

Ile Thr His Pro Pro Leu Asn Pro Glu His Phe Val Ser Arg Val Phe
1   5   10   15

Ser Ser Leu Gly Leu Lys Ser Tyr Gln Pro Lys Asp Asp Arg Phe Leu
            20   25   30

Arg Lys Pro Ser Asp Ser Arg His Pro Glu Ser Gly Asn Ser Gly Lys
        35   40   45

Trp Gln Val Leu Asn Ser Pro Leu Val Ile Val Lys
    50   55   60

<210> 268

<211> 30

<212> PRT

<213> Streptococcus pneumoniae

<400> 268

Thr Leu Ala Lys Ala Val Gly Leu Met Tyr Ser Pro Pro Ile Pro Pro
1   5   10   15

Lys Pro Phe Leu Gly Arg Ile Thr Thr Asp Ser Ser Ser Ile
            20   25   30

<210> 269

<211> 83

<212> PRT

<213> Streptococcus pneumoniae

<400> 269

Pro Gly Ser Pro Phe Ser Glu Ile Ser Gly Ala Gly Phe Phe Gly Val
1 5 10 15

Ala Lys Arg Ile Phe Pro Arg Pro Pro Arg Pro Pro Trp Ala Thr Ile
20 25 30

Asn Ser Cys Pro Cys Ser Ile Lys Ser Val Lys Thr Leu Pro Val Ser
35 40 45

Ala Ser Arg Thr Val Val Pro Cys Gly Thr Arg Thr Leu Arg Ser Ser
50 55 60

Ala Pro Arg Pro Cys Ile Pro Leu Val Ile Pro Phe Ser Pro Glu Ser
65 70 75 80

Ala Leu Lys

<210> 270

<211> 111

<212> PRT

<213> Streptococcus pneumoniae

<400> 270

Ile Asn Ser Leu Thr Leu Ala Thr Ser Leu Ser Lys Arg Arg Ala Pro
1 5 10 15

Arg Lys Ala Ser Lys Ala Ser Pro Arg Met Val Ser Arg Leu Arg Pro
20 25 30

Pro Asp Phe Ser Ser Pro Leu Pro Asn Leu Ile Asn Trp Ser Asn Trp
35 40 45

Gln Ser Arg Ala Lys Pro Ala Lys Leu Ser Ser Arg Thr Ile Ile Ala
50 55 60

Arg Ser Phe Asp Arg Ser Pro Ser Gly Phe Leu Gly Tyr Phe Leu Tyr
65 70 75 80

Arg Tyr Ser Glu Ile Asn Asn Cys Arg Thr Ala Ser Pro Lys Asn Ser
85 90 95

Lys Arg Ser Leu Cys Glu Ile Phe Lys Arg Arg Cys Ser Leu Ala
100 105 110

<210> 271

<211> 49

<212> PRT

<213> Streptococcus pneumoniae

<400> 271

Pro Ile Gly Lys Arg Asn Cys Lys Ala Glu Cys Gln Ser His His Leu
1 5 10 15

Leu Glu Lys Gln Lys Thr Phe Gln Ser Arg Lys Thr Lys Arg Tyr Gly
20 25 30

Ala Ser Pro Glu Pro Arg Tyr Arg Glu Ser Arg Lys Pro Arg Leu Ser
35 40 45

Gln

<210> 272

<211> 58

<212> PRT

<213> Streptococcus pneumoniae

<400> 272

Gln Pro Leu Gly His Ser Lys Ala Glu Glu His Glu Thr Ile Cys Ser
1 5 10 15

His Thr Phe Asp Asn His Thr Thr Glu Thr Ile Pro Asn Gln Val Lys
20 25 30

Gly Arg Asp Met Thr Ser Ser Glu Thr Leu Pro Phe Pro Ser Lys Asn
35 40 45

Gln Asn Gln Gly Lys Ala Lys Gln Ile Pro
50 55

<210> 273

<211> 125

<212> PRT

<213> Streptococcus pneumoniae

<400> 273

Pro Cys Ser Leu Pro Asp Tyr Gly Leu Val Gly Ser Gly Tyr His Ser
1 5 10 15

Cys His Tyr Gln Ser Asn Asp Thr Arg Phe Leu Glu Ser His Gly Asn
20 25 30

Trp Arg Thr Leu Leu Tyr Ser Trp Ser Trp Ile Leu Cys Gln Glu Lys
35 40 45

Thr Leu Phe Pro His Asp Leu Ala Ser Leu Tyr Pro Ser Cys Val Arg
50 55 60

Thr Ser Ile His Arg Tyr Cys Leu Leu His Val Lys Lys Leu Arg Asn
65 70 75 80

Ser Ile Ser Thr Phe Phe Phe Thr His Ile Asp Lys Val Leu Val Gln
85 90 95

Ala His Ile Ile Ser Gln Phe Trp Met Lys Arg Thr Tyr Gln His Ile
100 105 110

Phe Phe Leu Gly Cys Asn Asn Leu Ile Val His Cys Cys
115 120 125

<210> 274

<211> 69

<212> PRT

<213> Streptococcus pneumoniae

<400> 274

Arg Val Lys Asp Asn His Leu Asp Lys Leu Val Lys Ala Leu Leu Lys
1 5 10 15

Arg Arg Ser Ser Thr Gln Tyr Tyr Ile His Gln Leu Leu Arg Lys Met
20 25 30

Ile Arg Leu Tyr Gly His Gln Gln Leu His Asn Asn Ser Glu Ile Leu
35 40 45

Val Tyr Ser Asp Tyr Gly His Val Asp Leu Leu Leu Leu Glu Thr Asn
50 55 60

Lys Ile Pro Val Tyr
65

<210> 275

<211> 40

<212> PRT

<213> Streptococcus pneumoniae

<400> 275

Gln Val Ile Lys Ile Asp Ile Ala Thr Thr Asn Lys Thr Glu Ser Val
1 5 10 15

Lys Ser Gln Ser Glu Arg Glu Lys Lys Arg Leu Thr Ser Ser Asn Ile
20 25 30

Leu Lys Val Arg Gly Arg Pro Ile
35 40

<210> 276

<211> 32

<212> PRT

<213> Streptococcus pneumoniae

<400> 276

Ala Phe Lys Ser Ser Lys Val Pro Ser Leu Asp Pro Ser Ser Thr Lys
1 5 10 15

Thr Tyr Ser Ile Ser Val Ser Lys Ser Gly Ser Lys Ala Ser Arg Ala
20 25 30

<210> 277

<211> 69

<212> PRT

<213> Streptococcus pneumoniae

<400> 277

Asp Lys Thr Asp Pro Leu Ala Arg Lys Leu Pro Asp Lys Ser Lys Pro
1 5 10 15

Ser Thr Ser Phe Cys Thr Lys Ser Leu Ser Pro Val Asn Met Ala Ser
20 25 30

Leu Thr Ser Ala Lys Pro Ser Lys Thr Lys Ala Ser Leu Gly Ile Cys
35 40 45

Ser Pro Ala Asp Lys Arg Met Thr Ser Pro Ser Thr Asn Ser Ser Gly
50 55 60

Leu Arg Ala Thr Ser
65

<210> 278

<211> 38

<212> PRT

<213> Streptococcus pneumoniae

<400> 278

Leu Cys Arg Leu Gln Thr Gln Ala Arg Pro Arg Gly Ser Val Thr Asn
1 5 10 15

Leu Thr Lys Gln Asn Lys Val Tyr Arg Tyr Leu Asn Tyr Leu Arg Gln
20 25 30

Thr Gln Leu Ser Ala Met
35

<210> 279

<211> 110

<212> PRT

<213> Streptococcus pneumoniae

<400> 279

Cys Ile Gln Ser Ile Gly Asn Glu Gly Gln Cys Lys Gly Asn Ser Cys
1 5 10 15

Tyr Val Gly Lys Glu Ile His Leu Ala Pro Ile Ser Asp Ile Val Gly
20 25 30

His Lys Gly Lys Glu Glu Gly Asp Asp Gly Asn Asp Asp Gly Arg Gln
35 40 45

Phe Tyr Leu Phe Leu Ala His Leu Val Gly Ser Ala Phe Leu Arg Ser
50 55 60

Phe Pro Leu Leu Tyr Ser Lys Gly Ile Asn Glu Glu Gly Asp Gly Ile
65 70 75 80

Gly Asn Asp Gly Arg Leu Ile Ser Lys Asp Ile Ile Asn Ser Thr Gly
85 90 95

Gln Asn Gly Ile Asn Asn Thr Lys Val Ile Ser Pro Phe Ala
100 105 110

<210> 280

<211> 121

<212> PRT

<213> Streptococcus pneumoniae

<400> 280

Thr Ser Thr Lys Leu Val Ile Asp Thr Thr Thr Phe Met Thr Phe Cys
1 5 10 15

Thr Asn Asn Thr Lys Ser Ser Lys Phe Thr Asn Thr Phe Thr Lys Leu
20 25 30

Asp Val Gly Thr Thr Thr Arg His Val Gly Cys Asp Gly Asn Gly Thr
35 40 45

Thr Leu Thr Ser Ile His Asp Asp Leu Gly Phe Ser Ile Val Val Phe
50 55 60

Gly Ile Gln Asp Phe Val Arg Asn Thr Ser Cys Asn Gln Phe Leu Arg
65 70 75 80

Asn Val Val Thr Ser Phe Asn Arg Tyr Cys Thr Asn Gln Asp Arg Leu
85 90 95

Thr Leu Leu Val Thr Ser Leu Asn Val Phe Asp Asn Arg Phe Lys Leu
100 105 110

Arg Phe Asp Thr Cys Ile Lys Lys Val
115 120

<210> 281

<211> 27

<212> PRT

<213> Streptococcus pneumoniae

<400> 281

Ile Ser Thr Gly Val Pro Thr Cys Ser Met Tyr Pro Leu Leu Lys Thr
1 5 10 15

Ala Ile Leu Ser Asp Lys Val Lys Ala Ser Ser
20 25

<210> 282

<211> 34

<212> PRT

<213> Streptococcus pneumoniae

<400> 282

Leu Ser Thr Met Ser Ser Ile Lys Ser Ile Leu Cys Ser Leu Pro Thr
1 5 10 15

His Thr Ile Phe Ser Lys Ser Ala Ile Ser Pro Lys Arg Gly Ser Thr
20 25 30

Ala Ile

<210> 283

<211> 111

<212> PRT

<213> Streptococcus pneumoniae

<400> 283

Ser Cys Ser Tyr Ser Ser Thr Asn Ser Lys Ala Cys Ser Ile Val Gly
1 5 10 15

Leu Ser Lys Pro Thr Ile Phe Ile Cys Val Thr Pro Ile Ser Ala Ala
20 25 30

Lys Ala Ile Ser Ser Ala Ser Arg Pro Ala Asn Ser Ser Thr Phe Lys
35 40 45

Cys Val Cys Val Ser Lys Ile Ile Ser Ser Asn Leu Val Phe Tyr Leu
50 55 60

Leu Leu Tyr Gln Lys Arg Gly Gly Ala Pro Asn Phe Ser Val Ser Pro
65 70 75 80

Pro Leu Phe Asn Arg Glu Leu Phe Cys Tyr Leu Phe Tyr Pro Ile Leu
85 90 95

Pro Ile Ser Tyr Ser Thr Val Arg Asp Arg Arg Asp Trp Leu His
100 105 110

<210> 284

<211> 110

<212> PRT

<213> Streptococcus pneumoniae

<400> 284

Val Thr Ser Cys Ile Val Pro Ala Val Ala Cys Gly Ala Leu Val Val
1 5 10 15

Leu Gly Ala Ala Leu Gly Ala Thr Gly Leu Leu Gly Thr Val Thr Met
20 25 30

Ala Met Ala Cys Thr Pro Ile Val Ser Ala Ser Phe Thr Ser Ser Ile
35 40 45

Val Phe Ala Phe Ser Ile Ser Leu Arg Ala Ala Cys Phe Ser Ala Ser
50 55 60

Thr Leu Ala Lys Ser Ser Ala Phe Ser Leu Ser Glu Ser Gly Ala Pro
65 70 75 80

Leu Ile Ser Ser Cys Leu Ser Leu Ala Ala Phe Ser Met Ala Phe Leu
85 90 95

Ala Asp Ser Phe Ser Val Ala Asn Cys Leu Glu Ala Cys Asp
100 105 110

<210> 285

<211> 53

<212> PRT

<213> Streptococcus pneumoniae

<400> 285

Tyr Ser Pro Phe Asn His Ser Ile Leu Ile Arg Lys Thr Thr Lys Ile
1 5 10 15

Ile Asn Pro Asn Pro Lys Ala Pro Arg Met Asn Trp Arg Ser Lys Val
20 25 30

Trp Ser Asn Gln Pro Val Asn Ile Ser Thr Asn His Thr Lys Ser Asp
35 40 45

Arg Pro Ile Lys Lys
50

<210> 286

<211> 48

<212> PRT

<213> Streptococcus pneumoniae

<400> 286

Asp Tyr Phe Lys Phe Arg Thr Thr Phe Thr Arg Phe Ser Thr Val Lys
1 5 10 15

Pro Tyr Ser Ala Asn Thr Phe Gly Ala Gly Ala Glu Ala Pro Lys Val
20 25 30

Ser Ile Pro Arg Thr Ala Pro Ser Arg Pro Thr Tyr Leu Tyr Gln Phe
35 40 45

<210> 287

<211> 74

<212> PRT

<213> Streptococcus pneumoniae

<400> 287

Arg Gly Arg Arg Gly Leu Cys Val Ala Arg Ile Lys Ala Pro Arg Leu
1 5 10 15

Val Ile Lys Pro Lys Arg Thr Ile Asp Pro Pro Thr Lys Asp Arg Tyr
20 25 30

Ser Pro Pro Leu Ser Ala Thr Ser Leu Ser Val Pro Lys Ser Pro Ile
35 40 45

Ile Ser Phe Pro Ala Lys Met Asp Lys Asn Pro Lys Arg Lys Leu Asn
50 55 60

Ser Lys Val Ile Phe Asn Ala Ser Val Thr
65 70

<210> 288

<211> 30

<212> PRT

<213> Streptococcus pneumoniae

<400> 288

Thr Pro Pro Tyr Thr Lys Ile Pro Ala Lys Thr Ala Ile Ile Pro Phe
1   5   10   15

Ile Ser Ala Gln Asp Phe Asn Gln Ala Gln Arg Leu Ser Gly
            20   25   30

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